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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

July 12, 2005, 07:34:30 ; Search time 70 Seconds (without alignments) 5011.310 Million cell updates/sec

US-10-751-736-84 Title: Perfect score:

1 MDTSRLGVLLSLPVLLQLAT......PAYPVTESCHLSSVAFVPCL 907 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

2105692

length: 0 length: 2000000000 sed Minimum DB Maximum DB Maximum

Post-processing:

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

4: geneseqp2000s:*

5: geneseqp2001s:*

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7: geneseqp2003bs:*

8: geneseqp2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aaw93889 Human HG3	Aay90682 Human G p	Abp81968 Human G p	Abo06467 Human G-p	Adc22783 Human G p	Ade59150 Human Pro	Ade59153 Human Pro	Adg42628 Human G p	Adh14256 Human HG3	Adn40013 Cancer/an	Adn39531 Cancer/an	Adn39628 Cancer/an	Ado29408 Human GPC	Adq80369 G protein	_	Adf70480 Orphan re	Aay90687 Human mut	Adc22797 Human G p	Adh14270 Mutated h	Adg42629 Human G p	Adb80464 Ovarian c	Adn40012 Cancer/an	Adn39166 Cancer/an	Adg75449 Mouse orp	Ado29409 Mouse GPC
COLUMNIA	ID	AAW93889	AAY90682	ABP81968	AB006467	ADC22783	ADE59150	ADE59153	ADG42628	ADH14256	ADN40013	ADN39531	ADN39628	AD029408	ADQ80369	ADR67868	ADF70480	AAY90687	ADC22797	ADH14270	ADG42629	ADB80464	ADN40012	ADN39166	ADG75449	AD029409
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Aay42169 Human LGR Aaw93890 Human HG3 Aag66138 Mouse LGR	O 10 M	Adf70441 Orphan re Aag66141 Human LGR Adc16691 Human G-p		Human Human Human	Human Human	Human Novel
AAY42169 AAW93890 AAG66138	ADN02240 ADK19405 ADC16693	ADF70441 AAG66141 ADC16691	ADD89091 ADN02249	ADQ15074 ABJ37069 ADC16699	ADC16711 ADG42625 ADC16697	AAU79941 ADG42573
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ALIGNMENTS

HG38; human; G-protein coupled glycoprotein hormone receptor; brain; endocrine system; skeletal muscle; spinal cord; placenta; development; receptor activity modulator. AAW93889 standard; protein; 907 AA. (first entry) Human HG38 protein. 25-JUN-1999 Homo sapiens AAW93889; AAW93889

98WO-US019979. WO9915660-A1 24-SEP-1998; 01-APR-1999.

97US-0059863P. (MERI) MERCK & CO INC. 24-SEP-1997;

WPI; 1999-254711/21. N-PSDB; AAX23980.

Mcdonald TP;

Bailey WJ,

Liu Q,

Human G-protein coupled glycoprotein hormone receptor HG38. Claim 1a; Fig 2; 74pp; English. This invention describes a novel human G-protein coupled glycoprotein hormone receptor. HG38. Glycoprotein hormone receptors are important in the endocrine system and HG38 may be involved in development and function of the skeletal muscle, spinal cord, placenta and to a lesser extent, the brain. The transgenic animal may be useful for studying tissue and temporal specific expression or activity of the HG38 receptor, as well as for studying the ability of a variety of compounds to act as modulators of HG38 receptor activity

Sequence 907 AA;

'DB 2; Length 907; Score 4702; Pred. No. 0; 100.0%; Query Match Best Local Similarity 21-AUG-2000 (first entry)

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AAY90682 standard; protein; 907 AA.

AAY90682

RESULT 2
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The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-CAAY90647 and AAY906843-A90684), and to DNA encoding them (AAA3079-A30743) and AAA30775-A30779). The mutant proteins of the invention contain a contain a mataion of the protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TM6). A non-endogenous anino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acid 8 N-terminal of an endogenous proline in IC3 at a position 16 amino acid 8 N-terminal of an endogenous proline in IC3 at a position 16 acids N-terminal of an endogenous proline in IC3 at a position 16 acids N-terminal of an endogenous proline in IC3 at a position 16 acids N-terminal of an endogenous proline in IC3 at a position 16 acids N-terminal of an endogenous proline in IC3 at a position 16 acids N-terminal of an endogenous proline in IC3 at a position 16 acids N-terminal of acids stretch between the substituted amino acid and the Pro may be endogenous, non-endogenous, or a mixture of endogenous and non-endogenous cresidues. The constitutively active GPCRs are useful for identifying antagonists and partial agonists for use as pharmaceutical containing the roles of the receptors in normal and diseases and disorders associated with that receptors in normal and diseases and compounds without the need for endogenous ligands. The present sequence corpusion of the invariant processing the in an exemplification of the invariant processing the compounds without the need for endogenous ligands. The present sequence the invariant processing the compounds without the need for endogenous ligands. The present sequence the invariant processing the constitution of the processing the constitution of the constitutio
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                                                                                    3 protein-coupled receptor; GPCR; constitutively active;
intracellular loop 3; transmembrane domain 6; drug screening; agonist;
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                                      Human G protein-coupled receptor HG38.
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Matches 907; Conservative
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                                            LNYNNLDEPPTAIRTLSNLKELGFHSNNIRSIPEKAFVGNPSLITIHFYDNPIQFVGRSA
                                                                                        FQHLPELRTLTLNGASQITEPPDLTGTANLESLTLTGAQISSLPQTVCNQLPNLQVLDLS
                                                                                                                                                   YNLLEDLPSFSVCQKLQKIDLRHNEIYEIKVDTFQQLLSLRSLNLAWNKIAIIHPNAFST
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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino conditions. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a capdidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for carearing immune-related diseases, growth-related cell proliferative comparation-related diseases, immunological-related cell proliferative diseases, autoimmune diseases, immunological-related cell proliferative diseases, bacterial fungal, photozoan or viral infections, atherostribritis, osteoporosdia, cancer, cardiomyopathy, chronic and acute inflammation, allergies, CPCPM-adiabetes, graft versus host disease, parkinson's disease, multiple sclerosis, pain, psoriasis, concertions and such antibodies may be used in immunoaseaye and immunodiagnosis, ABP82123 to AB242869 encode GPCR proteins given invention invention (GPCR proteins given invention invention).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
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                                                                     FQHLPELRTLTLNGASQITEFPDLTGTANLESLTLTGAQISSLPQTVCNQLPNLQVLDLS
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The invention relates to an isolated HGPRBMYS polypeptide. The polypeptides, polynucleotides and methods are useful for preventing, treating or ameliorating a medical condition such as a neoplastic disorder e.g. leukaemia and breast cancer; immune disorder e.g. Alzheimer's disease and renumatoid arthritis; neuronal disorder e.g. Alzheimer's disease and parcosast's syndrome; ovaryan disorder e.g. bronchopulmonary disease and pancosast's syndrome; ovaryan disorder e.g. ovarian carcinoma and meig's syndrome; colon disease, breast disease; thalamus related disorder; amygdala related disorder; gorpus callosum related disorder; caudate nucleus related disorder; hippocampus related disorder by administering the GPCR polypeptide or its homologue. The present sequence represents the amino acid sequence of a G-protein coupled receptor used to show homology with the human G-protein coupled receptor, HGPCRBMY
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                                             27-SEP-2000; 2000US-0235832P.
16-JAN-2001; 2001US-0261781P.
19-JUL-2001; 2001US-0306605P.
03-AUG-2001; 2001US-0310436P.
26-SEP-2001; 2001US-00965536
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The invention relates to a method for treating a non-endogenous, constitutively active version of an endogenous human G protein-coupled receptor (GPCR) that has a transmembrane 6 (TWG) region and an intracellular-3 (TG3) region, by substituting a specific amino acid in the TWG region with a different amino acid, and testing for constitutive activity. The method is useful for creating a constitutively active version of an endogenous human GPCR that comprises a transmembrane 6 region and an intracellular loop 3 region. The altered human GPCR polypeptides are useful for sorreming test compounds for identification of inverse agonists or partial agonists of GPCR polypeptides, which may have therapeutic uses. The altered GPCRs may also be used in vivo or in troi in biological research. A nucleic acid encoding the altered GPCR may be used to create a transgenic animal expressing the altered GPCR. The method allows screening for compounds that modulate the activity of human G protein-coupled receptor without the need for provision of a ligand for the receptor. This is particularly useful in allowing screening of compounds against orphan receptors for which no ligand is currently known. This sequence represents a human GPCR polypeptide of the
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The invention discloses a composition comprising two or more isolated rat or human polynuclectides or a polynuclectide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynuclectide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the
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                                                                           STMGYMVALILLINSLCFLMMTIAYTKLYCNLDKGDLENIWDCSMVKHIALLLFTNCILNC
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spinal segmental nerve injury, chronic constriction injury, CCI,
spared nerve injury, SNI, Chung.
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(FARB ) BAYER AG.
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polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
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The invention discloses a composition comprising two or more isolated rate or human polymucleotides or a polymucleotide which represents a fragment, derivative or allelic variation of the mucleic acid sequence. Also claimed are a vector comprising the movel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a gent to particular the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially compound that regulates the activity of one or more of the polymucleotides, a method for producing a pharmaceutical composition, a compound that regulates the activity of one or more of the polymetides given in the specification, a method for identifying a compound or small molecule that regulates the cativity in an animal of one or more of the polymetides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polymetides or their antibodies. The polymucleotide or the compound that compound that modulates its activity is useful for preparing a medicament for treating modulates its activity is useful for preparing a medicament for treating modulates its activity is useful for preparing a medicament for treating
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spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
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injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene, therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the posinted specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes a new isolated polypeptide comprising: a polypeptide or its mature form comprising a sequence not given in the specification; or a variant of (A), where one or more amino acid residues in the variant differs in no more than 15% from the amino acid sequence of the mature form. The pharmaceutical composition may be administered via oral, transdermal, rectal or parenteral route. The polypeptide, nucleic acid or antibody is useful for preparing a composition for treating or preventing a NOVA-associated disorder, e.g. cancer. This is the amino acid sequence of a transmembrane receptor homologue used in a comparison with the novel human proteins of the invention.
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                                                                                                                                                                                                                                                                                                                                                            cytostatic, gene therapy, NOVX-agonist, NOVX-antagonist, pharmaceutical, NOVX-associated disorder, cancer, human, G protein coupled receptor 49.
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                                                                                                                                                                                                                                                                                                                 Human G protein-coupled receptor 49
                                                                                                                                                                    ADG42628 standard; protein; 907 AA
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(RAST/) RASTELLI L.
(SHIM/) SHIMKETS R A.
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Human; differential expression; cancer; angiogenic disorder; fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine.
                                             RIGESVKYSAKFETKAPFSSEKVIILLCALLALTMAAVPLLGGSKYGASPLCLPLPFGEP
                                                                                                                                                                                                                           STMGYMVALILLNSLCFLMMTIAYTKLYCNLDKGDLENIWDCSMVKHIALLLFTNCILNC
                                                                                                                                                                                                                                                        STMGYMVALILIANSLCFLAMTIAYTKLYCNLDKGDLENIWDCSMVKHIALLLFTNCILNC
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12-APK-2002; 2002US-0372246P.
05-UUN-2002; 2002US-0386614P.
16-UUL-2002; 2002US-0386614P.
22-TTT
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29-NOV-2001; 2001US-0332464P.
29-NOV-2001; 2001US-0335394P.
14-DEC-2001; 2001US-0335394P.
14-DEC-2001; 2001US-0335394P.
10-JAN-2002; 2002US-0347311P.
10-JAN-2002; 2002US-0347349P.
08-PEB-2002; 2002US-0347349P.
29-PEB-2002; 2002US-0355250P.
29-MAR-2002; 2002US-0359077P.
29-MAR-2002; 2002US-0358809P.
04-APR-2002; 2002US-0358809P.
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                                                                                                                                                                                                                                                                                New constitutively active, non-endogenous version of an endogenous human G protein-coupled receptor for the identification of therapeutic compounds, such as agonists.
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100.0%; Pred. No. 0;
ive 0; Mismatches
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                                                                                                                                                     Chalmers
98US-00170496
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                                                                                                                                                     Liaw CW, Behan DP,
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Best Local Similarity
Matches 907; Conserv
                                                                                                  (CHAL/) CHALMERS D
                                                LIAW C W.
BEHAN D P.
                                                                                                                                                                                                                                   N-PSDB; ADH14255
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13-OCT-1998;
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Human, differential expression, cancer; angiogenic disorder;
fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
inflammatory disease; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                               AVNMLTGVSSAVLAGVDAFTFGSFARHGAWWENGVGCHVIGFLSIFASESSVFLLTLAAL
                                                                                                                                                                                         721 STWGYWVALILLINSLCFLMMTIAYTKLYCNLDKGDLENIWDCSWVKHIALLLFTNCILNC
                                                                                                                                                                                                                                                                                                                                                                                                                              WTRSKHPSLMSINSDDVEKQSCDSTQALVTFTSSSITYDLPPSSVPSPAYPVTESCHLSS
                                                                     601 AVNMLTGVSSAVLAGVDAFTFGSFARHGAWWENGVGCHVIGFLSIFASESSVFLLTLAAL
                                                                                                                                                             ERGFSVKYSAKFETKAPFSSLKVIILLCALLALTMAAVPLLGGSKYGASPLCLPLPFGEP
                                                                                                                                                                                                                                                   STMGYMVALILLNSLCFLMMTIAYTKLYCNLDKGDLENIWDCSMVKHIALLLFTNCILNC
                                                                                                                                                                                                                                                                                                                                        PVAFLSFSSLINLTFISPEVIKFILLVVVPLPACLNPLLYILFNPHFKEDLVSLRKQTYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    retinal neovascularistaton syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine.
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2001US-0332464P.
2001US-0335394P.
2001US-0340376P.
2002US-0347211P.
2002US-03473149P.
2002US-035526P.
2002US-035514P.
2002US-0359077P.
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2002US-0397775P.
2002US-0397845P.
2002US-0409450P.
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2002US-0372246P.
2002US-0386614P.
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03-DBC-2001;
04-DBC-2001;
08-JAN-2002;
10-JAN-2002;
08-FBB-2002;
20-FBB-2002;
20-FBB-2002;
20-FBB-2002;
20-FBB-2002;
20-FBB-2002;
20-FBB-2002;
20-FBB-2002;
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                                                                                                                                                                                                                                                                The invention relates to nucleic acids and proteins (ADN38683-ADN40464)

whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a mucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drageting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistation syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present
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                                                                                                                                                               useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                        Determining the presence or absence of a pathological cell in a patient
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      Hevezi I
A;
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    Gish KC, Glynne R,
Wilson KE, Zlotnik
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                                                                                                                                                                                                                              Claim 12; SEQ ID NO C383; 1385pp; English.
    Aziz N, Ginsburg WM,
Murray R, Watson SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·
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                                                                     2003-468649/44.
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                                                                                          N-PSDB; ADN39796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 907 AA;
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Best Local S
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The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
other diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
patient by detecting a mucleic acid at least 80% identical to those of
the invention or by detecting a polypeptide of the invention. The
invention also relates to expression vectors and host cells comprising a
nucleic acid of the invention; use of such antibodies for drug targeting;
and methods of screening for modulators of activity or expression of the
polypeptides and nucleic acids. The nucleic acids, polypeptides,
antibodies and methods are useful for diagnosing, prognosing and treating
cancer and other conditions such as psoriasis, ischaemia, heart disease,
attherosclerosis, inflammators of serving and uterine fibroids. They may
also be useful in wound healing and in contraception. The present
sequence represents a polypeptide of the invention.
                                                                                                                                     Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                Gish KC, Glynne R, Hevezi PA;
Wilson KE, Zlotnik A;
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100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                            Claim 12; SEQ ID NO A131; 1385pp; English.
                                Ginsburg WM,
R, Watson SR,
EOS BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 907; Conservative
                                                 Murray R,
                                                                                    2003-468649/44.
                                Aziz N,
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DB 7; Length 907;
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2001US-0335394P. 2001US-0340376P. 2002US-0347211P. 2002US-0355250P. 2002US-0356714P. 2002US-0359077P. 2002US-0359077P. 2002US-0370110P. 2002US-03702110P.

08-JAN-2002; 10-JAN-2002; 08-FEB-2002; 13-FEB-2002; 20-FEB-2002;

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2002US-0396839P. 2002US-0397775P. 2002US-0397845P.

22-JUL-2002;

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2001US-0332464P. 2001US-0334393P.

-DEC-2001;

2001US-0350666P 2002WO-US036810

13-NOV-2002;

22-MAY-2003

WO2003042661-A2.

Homo sapiens.

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          BRGFSVKYSAKFETKAPFSSLKVIILLCALLALTWAAVPLLGGSKYGASPLCLPLPFGEP
                                                                                                                                       STWGYWVALILLINSLCFLMMTIAYTKLYCNLDKGDLENIWDCSMVKHIALLLFTNCILNC
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                                        AVNMLTGVSSAVLAGVDAFTFGSFARHGAWWENGVGCHVIGFLSIFASESSVFLLTLAAL
                                                                                 ERGFSVKYSAKFETKAPFSSLKVI ILLCALLALTMAAVPLLGGSKYGASPLCLPLPFGEP
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                                                                                                                                                            Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
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Wilson KE,
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100.0%; Pred. No. 0;
iive 0; Mismatches
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                                                              Ginsburg WM,
R, Watson SR,
                                 EOS BIOTECHNOLOGY INC
 09-SEP-2002; 2002US-0409450P.
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Matches 907; Conservative
                                                                Afar D, Aziz N, Gin
Mack DH, Murray R,
                                                                                                               WPI; 2003-468649/44.
N-PSDB; ADN39627.
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KX

KW G protein-coupled receptor; GPCR; drug screening; diagnosis;

KW transgenic mouse; neurological disorder; adrenal(gland disorder;

KW transgenic mouse; neurological disorder; adrenal(gland disorder;

KW colon disorder; intestinal disorder; immune disorder; bone disorder;

KW joint disorder; metabolic disorder; nutritive disorder; cancer;

KW joint disorder; liver disorder; lung disorder; breast disorder;

KW skin disorder; liver disorder; prostate disorder; spleen disorder;

KW skin disorder; thyroid disorder; antiparkinsonian; antimanic;

CM stocentral nervous system; respiratory; antidiarbhoeic; antidiabetic;

W CMS; central nervous system; respiratory; antidiabetic;

W CMS; central nervous system; respiratory; antidiabetic;

W inmuniosuppressive; natiulcer; antithyroid; antiallergic; anorectic;

W immunosuppressive; human;

W immunosuppressive; human;
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Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H;
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The invention relates to human and mouse G protein-coupled receptors

(GPCRs) and nucleic acids encoding them. The invention also relates to

sequences at least 90% identical to the GPCR proteins and nucleic acids

of the invention; methods of treating, preventing and nucleic acids

of the invention; methods of treating, preventing or diagnosing diseases

compounds useful in the treatment of GPCR related diseases, a transgenic

compounds useful in the treatment of GPCR related diseases, a transgenic

compounds useful in the invention; methods of screening for

mutation in a GPCR gene of the invention; a mouse comprising

compounds useful in the treatment of GPCR related diseases, a transgenic

compounds useful in the transgene or in an endogenous GPCR gene; cells derived

compound in a different GPCR gene of the invention; and kits comprising

a mutation in a different GPCR gene of the invention. The

compound in a different GPCR gene of the invention. The

compound in a different GPCR gene of the invention. The

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confidences of the adrenal gland; disorders of the colon or intestine

compound in infarction); muscular disorders (e.g., autoimmune disorders or

consocial infarction); muscular disorders (e.g., autoimmune disorders or

consocial infarction); muscular disorders (e.g., autoimmune disorders (e.g., ansemia or lenkaemia); immune disorders (e.g., autoimmune disorders (e.g., anterial contre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases); and disorders of the kidney, liver, lung, breast, ovary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence repersents a GPCR of the invention. Note: The full sequence data for this patent did not form part of the printed specification; those sequences not shown were obtained in
                                                                                                                          Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina
                                                                                                                                                                                                                                                                                                          Claim 151; SEQ ID NO 510; 542pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                   pectoris, Parkinson's disease.
                               2004-390329/36
                                                                  N-PSDB; ADO29923.
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DB 8; Length 907; Query Match
100.0%; Score 4702;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 907; Conservative 0; Mismatches Sequence 907 AA;

ö 9 1 MDTSRLGVLLSLPVLLQLATGGSSPRSGVLLRGCPTHCHCEPDGRMLLRVDCSDLGLSEL Gaps ö Indels ö

9 1 MDTSRLGVLLSLPVLLQLATGGSSPRSGVLLRGCPTHCHCEPDGRMLLRVDCSDLGLSEL

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181 APRSLSALQAMTLALNKIHHIPDYAPGNLSSLVVLHLHNNRIHSLGKKCFDGLHSLETLD

360 PQHLPELRTLTLNGASQITEFPDLTGTANLESLTLTGAQISSLPQTVCNQLPNLQVLDLS 360 FQHLPELRTLTLINGASQITEFPDLTGTANLESLTLTGAQISSLPQTVCNQLPNLQVLDLS 301

900 480 480 540 540 900 900 9 9 720 720 780 840 840 900 361 YNLLEDLPSFSVCQKLQKIDLRHNEIYEIKVDTFQQLLSIRSLNLAWNKIAIIHPNAFST LPSLIKLDLSSNLLSSFPITGLHGITHLKLTGNHALQSLISSENFPELKVIEMPYAYQCC AFGVCENAYKI SNOWNKGDNSSMDDLHKKDAGMFQAQDERDLEDFLLDFEEDLKALHSVQ AFGVCENAYKI SNQWNKGDNSSMDDLHKKDAGMFQAQDERDLEDFILDFEEDLKALHSVQ CSPSPGPFKPCEHLLDGWLIRIGVWTIAVLALTCNALVTSTVFRSPLYISPIKLLIGVIA AVNMLTGVSSAVLAGVDAFTFGSFARHGAWWENGVGCHVIGFLSIFASESSVFLLTLAAL LPSLIKLDLSSNLLSSFPITGLHGLTHLKLTGNHALQSLISSENFPELKVIEMPYAYQCC CSPSPGPFKPCEHLLDGWL1R1GVWT1AVLALTCNALVTSTVFRSPLY1SP1KLL1GV1A AVNMLTGVSSAVLAGVDAFTFGSFARHGAWWENGVGCHVIGFLSIFASESSVFLLTLAAL **ERGFSVKYSAKFETKAPFSSLKVIILLCALLALTMAAVPLLGGSKYGASPLCLPLPFGEP** ERGFSVKYSAKPETKAPPSSLKVIILLCALLALTMAAVPLLGGSKYGASPLCLPLPPGEP STMGYMVALILLINSLCFLMMTIAYTKLYCNLDKGDLENIWDCSMVKHIALLLFTNCILNC PVAFLSFSSLINLTFISPEVIKFILLVVVPLPACLNPLLYILFNPHFKEDLVSLRKQTYV YNLLEDLPSFSVCQKLQKIDLRHNEIYEIKVDTFQQLLSLRSLNLAWNKIAIIHPNAFST 907 VAFVPCL 907 421 481 481 541 541 601 601 661 661 721 721 781 781 901 901 421 임 원 ò 유 셤 ò 셤 ò 셤 ò 셤 ò 요 ò 유 ଚ ઠે à

G protein-coupled receptor 49 protein, ADQ80369 standard; protein; 907 AA. (first entry 21-0CT-2004 ADQ80369; ADQ80369

RESULT 14

modulator; identification; response; cancer; EGFR; biomarker. Cytostatic, epidermal growth factor receptor therapeutic response; cancer; BGFR; biomarker WO2004063709-A2. Homo sapiens.

2003US-0438735P. BRISTOL-MYERS SQUIBEN 08-JAN-2004; 2004WO-US000368 T-Januario-T WPI; 2004-544114/52. 08-JAN-2003; Amler LC, (BRIM ()

240

29-JUL-2004.

Identifying a mammal that will respond therapeutically to a method of treating cancer comprises comparing the level of a biomarker in a mammal

N-PSDB; ADQ80249

780 780 840 900

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The invention relates to a method of identifying a mammal that will respond therapeutically to a method of treating cancer by administering an epidermal growth factor receptor (EGPR) modulator by comparing the level of a biomarker in a mammal before and after exposure to an EGPR modulator. The method comprises: (a) measuring, in the mammal, the level of a least one biomarker identified in the specification; (b) exposing the mammal to the EGPR modulator; and (c) measuring in the mammal the level of the biomarker, where a difference in the level in step (c) compared to step (a) indicates that the mammal will respond therapeutically to the method of treating cancer. The method and biomarkers are useful for identifying a mammal that will respond therapeutically to a method of treating cancer by administering an epidemal growth factor receptor (EGFR) modulator. This sequence corresponds to one of the biomarkers whose levels of expression is measured in the method of the invention.
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                                                        Disclosure; SEQ ID NO 141; 520pp; English
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known as HG38. The HG38 protein and corresponding nucleic acid, may be used in the method of the invention for detecting colon or lung cancer.

The first method involves performing an assay to determine the amount of HG38 in a sample of colon or lung tissue, and comparing the amount of protein to standard, thus detecting expression of protein in sample, where differential expression of protein in sample when compared with the involves hybridizing a composition comprising the HG38 coding sequence, or its complement, and a labelling moiety, to nucleic acids of a sample of comparing complex, detecting hybridization complex formation to a standard, where the comparison reflects the standard and is diagnostic of a colon or lung cancer. This first method enables earlier diagnosis before the pattent is symptomatic. Anti-HG38 antibodies are useful for treating colon or lung cancer.
ERGFSVKYSAKFETKAPFSSLKVIILLCALLALTMAAVPLLGGSKYGASPLCLPLPFGEP 720
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Search completed: July 12, 2005, 07:37:49 Job time : 80 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

July 12, 2005, 07:34:30 ; Search time 104 Seconds (without alignments) 4465.921 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-751-736-84 4702 1 MDTSRLGVLLSLPVLLQLAT......PAXPVTESCHLSSVAFVPCL 907

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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GO; GO:0005887; C:integral to plasma membrane; TAS.

RO; GO:0004930; F:G-protein coupled receptor activity; TAS.

RO; GO:0004930; F:G-protein coupled receptor activity; TAS.

RO; GO:000786; F:G-protein coupled receptor protein signalin. .; TAS.

InterPro; IPR002131; Gphrm. receptor.

InterPro; IPR002131; Gphrm. receptor.

R InterPro; IPR003591; LRR.

R Ffam; PF00650; LRR.

R Ffam; PF00650; LRR.

R Ffam; PF00650; LRR.

R Ffam; PF00462; LRRNT; 1.

R RINTS; PR00373; GLYCHORMONER.

R RINTS; PR00373; GLYCHORMONER.

R SMART; SM00369; LRR TYP; 8.

R SMART; SM00313; LRRNT; 1.

R ROSITE; PS00237; G PROTEIN RECEP F1 1; FALSE NEG.

R ROSITE; PS00237; G PROTEIN RECEP F1 2; 1.

R G-protein coupled receptor; Glycoprotein; Leucine-rich repeat; Repeat;

STANA.

SIGNAL: Transmembrane.
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coupled receptor 5.
Extracellular (Potential).
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Pred. No. 5.2e-272;
Mismatches 0; Indels 0;
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Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential).
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Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential).
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Cytoplasmic (Potential).
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Cytoplasmic (Potential).
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-> W (in Ref. 2).
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Leucine-rich repeat-containing G protein-coupled receptor 5 precursor (G protein-coupled receptor 49) (Orphan G protein-coupled receptor Name=Gpr49; Synonyms=Fex, Lgr5; Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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                                                                                                                                                    embryonic tissues.

--- SUBCELLUIAR LOCATION: Integral membrane protein.
--- TISSUE SPECIFICITY: Expressed in the gonads, the adrenal gland, and in the brain. In the central nervous system expression is restricted to the olfactory bulb. In the adrenal gland detected only in the neural-creat derived chromomaffin cells of the medulla, but not in the calls of the adrenal cortex. In the gonads, the expression is high in Graafian follicle, but absent from primary and secondary follicles.
--- DEVELOPMENTAL STAGE: Expressed from embryonic day 10.5 (E10.58) in the developping spinal cord and in the neuroepipithelia of the myel-, met-, mes-, and diencephalon. Expression is transitory and the pattern changed rapidly.
--- SIMILARITY: Balongs to the G-protein coupled receptor 1 family.
--- SIMILARITY: Contains 17 leucine-rich (IRR) repeats.
                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0373; GLYCHORMONER.
PRINTS; PRO0237; GPERHODOPSN.
PRINTS; PRO019; LEURICHRPT.
SMART; SM0013; LRR TYP; B.
SMART; SM0013; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
SMART; PS050262; G PROTEIN RECEP_F1_1; FALSE_NEG.
G-protein coupled receptor; Glycoprotein; Leucine-rich repeat; Repeat;
                                                       MEDLINE 9912127; PubMed=9920770; DOI=10.1006/bbrc.1998.9882; Hermey G., Methner A., Schaller H.C., Hermans Borgmeyer I.; Hermety G., Methner A., Schaller H.C., Hermans Borgmeyer I.; aldentification of a novel seven-transembrane receptor with homology to glycoprotein receptors and its expression in the adult and developing mouse "; Biochem. Biophys. Res. Commun. 254:273-279(1999).

FINCTION: Orphan receptor. It may be an important receptor for signals controlling growth and differenciation of specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leucine-rich repeat-containing G protein-
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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2 (Potential).
Extracellular (Potential)
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Extracellular (Potential)
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or send an email to license@isb-sib.ch).
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InterPro; IRR000276; GPCR_Rhodpsn.
InterPro; IRR00131; Gphrmn_receptor.
InterPro; IRR001611; LRR.
InterPro; IRR00372; LRR_Nterm.
InterPro; IRR003591; LRR_typ.
Fam; PF000001; 7tm_1; 1.
Fam; PF00560; LRR; 16.
Pfam; PF01462; LRRNT; 1.
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SIGNAL 1
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LERR 4.
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LERR 6.
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LERR 7.
LERR 10.
LERR 11.
LERR 11.
LERR 13.
LERR 13.
LERR 14.
LERR 14.
LERR 14.
LERR 15.
LERR 16.
LERR 17.
N-linked (GlCNAC. . . ) (Potential) .
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; Pred. No. 5.4e-233;
53; Mismatches 78; Indels (
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             lasmic (Potential)
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85.6%;
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Matches 776; Conservative
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                                                                                             240 GNPLLQTIHFYDNPIQFVGRSAFQYLPKLHTLSLNGAMDIQEFPDLKGTTSLBILTLTRA
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SEQUENCE FROM N.A.

TISSUE=21308257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Staplecon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P.,

Brownstein N.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,
                                                                GNPSLITIHFYDNPIQFVGRSAFQHLPELRTLTLNGASQITEFPDLTGTANLESLTLTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GMFQAQDE----RDLEDFLLDFEEDLKALHSVQCSPSPGPFKPCEHLLDGWLIRIGVWTI
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                             SGLHSLRHLWLDDNALTEIPVQAFRSLSALQAMTLALNKIHHIPDYAFGNLSSLVVLHIH
         ERGFSVKYSAKFETKAPFSSLKVIILLCALLALTMAAVPLLGGSKYGASPLCLPLPFGEP
                                         ERGFSVKCSSKFEVKAPLFSLRAIVLLCVLLALTIATIPLLGGSKYNASPLCLPLPFGEP
                                                                                                                                                                                                                                                    PVAFLSFSSLINLTFISPEVIKFILLVVVPLPACLNPLLYILFNPHFKEDLVSLRKQTYV
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Ckaze H., Hayashi A., Kozuma S., Saito T.;

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB049405; BAB39854.1;

R HSSP; P25147; 1D0B.

GO; GO:0016021; Cintegral to membrane; IEA.

GO; GO:0016500; F:protein-hormone receptor activity; IEA.

GO; GO:0016500; F:protein-hormone receptor protein signalin...

R InterPro; IPR001211; GRR. Rhodpsn.

InterPro; IPR001211; LRR.

InterPro; IPR001211; LRR.

InterPro; IPR001511; LRR.

InterPro; IPR001511; LRR.

InterPro; IPR001511; LRR.

R PRINTS; PR00137; GEVERHODOPSN.

R PRINTS; PR00137; GEVERHODOPSN.

R RINTS; RR0019; LEURICHAPT.

R SMART; SM00169; LRR TYP; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
VTS20631 (Fragment).
Name=VTS20631,
Homo sepiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
11 TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             928 AA; 100487 MW; 4C3364ADEA89C463 CRC64;
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915 AA; 99265 MW;
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InterPro; IPR003591; LRR typ.
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PRINTS; PR00373; GLYCHORMONER.
PRINTS; PR00237; GPCRRHODOPSN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00365; LRR_SD22; 5.
SMART; SM00369; LRR_TYP; 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001611; LRR.
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47
                                                                                                                                                                                                                                                                                                                                                                                                   . .; IEA.
Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Kodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; Greet than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DTFQQLLSLRSLNLAWNKIAIIHPNAFSTLPSLIKLDLSSNLLSSFPITGLHGLTHLKLT
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R GO; GO:0016500; F:protein-hormone receptor activity; IEA.
GO; GO:00186; P:G-protein coupled receptor protein signalin. .;
R InterPro; IPR002131; Gphrmu_receptor.
R InterPro; IPR002131; Gphrmu_receptor.
R InterPro; IPR003191; IER.
R InterPro; IPR003191; IER.
R Pfam; PF00560; IER 1; 15.
R PRINTS; PR00319; GLYCHORMONER.
R PRINTS; PR00319; GLYCHORMONER.
R PRINTS; PR00319; LEURLHEPT.
R SWART; SW00369; IER_TYP; 8.
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                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC047905; AAH47905.1; -.
HSSP; Q9BZR6; IPBT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           923 AA; 100047 MW; 541D6746DAB06813 CRC64;
                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                 and mouse cDNA sequences."
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."; Genome Res. 13:2265-2270(203).

EMBL; AY358119; AAQ88486.1; -. GO; GO:0016521; C:integral to membrane; IRA.

GO; GO:0016521; F:integral to membrane; IRA.

GO; GO:0016501; F:protein-hormone receptor activity; IRA.

GO; GO:000186; P: P:G-protein coupled receptor protein signalin. .; IRA.

InterPro; IPR00276; GPCR Rhodsn.

InterPro; IPR00211; Gphrmn_receptor.
                                                                                                                                    TFGSFARHGAWWENGVGCHVIGFLSIFASESSVFLLTLAALERGFSVKYSAKFETKAPFS
RIGVWTIAVLALTCNALVTSTVFR-SPLYISPIKLLIGVIAAVNMLTGVSSAVLAGVDAF
                                     SLKVIILLCALLALTMAAVPLLGGSKYGASPLCLPL--PFGEPSTMGYMVALILLNSLCF
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Last annotation update)
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                                  GRMLLRVDCSDLGLSELPSNLSVFTSYLDLSMNNISQLLPNPLPSLRFLEELRLAGNALT 103
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                                                                                                    LRHIWLDDNALTEI PVQAFRSLSALQAMTLALNKIHHIPDYAFGNLSSLVVLHLHNNRIH 223
                                                                                                             SLGKKCFDGLHSLETLDLNYNNLDEFPTAIRTLSNLKELGFHSNNIRSIPEKAFVGNPSL 283
                                                                                                                                                284 ITIHFYDNPIQFVGRSAFQHLPELRTLTLNGASQITEFPDLTGTANLESLTLTGAQISSL 343
                                                                                                                                                                                 PQTVCNQLPNLQVLDLSYNLLEDLPSFSVCQKLQKIDLRHNEIYEIKVDTFQQLLSLRSL 403
                                                                                                                                                                                                                    NLAWNKIAIIHPNAFSTLPSLIKLDLSSNLLSSPPITGLHGLTHLKLTGNHALQSLISSE 463
                                                                                                                                                                                                                                                                                             SFPKLRILEVPYAYOCCPYGMCASFFKASGOW-----BAEDLHLDDEESSKRPLGLLAR 465
                                                                                                                                                                                                                                                                                                                    TCNALVTSTVFR-SPLYISPIKLLIGVIAAVNMLTGVSSAVLAGVDAFTFGSFARHGAWW 631
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09BXB1; 09NYD1;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-CTT-2004 (Rel. 45, Last annotation update)
Leucine-rich repeat-containing G protein-coupled receptor 4 precursor
                 Gaps
                 40;
Length 915;
tch 51.3%; Score 2410; DB 2; Length 9 al Similarity 54.7%; Pred. No. 2.8e-135; 480; Conservative 130; Mismatches 227; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Kes. Commun. 282:757-764(2001).

-!- FUNCTION: Orphan receptor.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- TISSUB SPECIFICITY: Expressed in multiple steroidogenic tissues:

-placenta, ovary, testis and adrenal. Expressed also in spinal cord, thyroid, stomach, trachea, heart, pancreas, kidney, prostate
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PRINTS; PRO0373; GPCRHODDPSN.
PRINTS; PRO0019; LEURICHRPT.
SMART; SMO0019; LRR TYP; 1.
SMART; SMO0019; LRR TYP; 4.
SMART; SMO0169; LRR TYP; 4.
G-protein coupled receptor; Glycoprotein; Leucine-rich repeat; Repeat; G-protein coupled receptor; Glycoprotein; Leucine-rich repeat; Repeat; Signal; Transmembrane.
Signal; Transmembrane.
SIGNAL
25 951 Leucine-rich repeat-containing G protein-chain
                                                                                                                                                                                                                                                                                                                                                                                                            Loh E.D., Broussard S.R., Kolakowski L.F. Jr.; "Molecular characterization of a novel glycoprotein hormone G-protein-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and spleen.
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
-!- SIMILARITY: Contains 15 leucine-rich (LRR) repeats.
                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                 TISSUE=Pancreas;
MEDLINE=21294803; PubMed=11401528; DOI=10.1006/bbrc.2001.4625;
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Bxtracellular (Potential).
Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential).
Cytoplasmic (Potential).
Cytoplasmic (Potential).
6 (Potential).
Cytoplasmic (Potential).
7 (Potential).
Cytoplasmic (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF346711; AAK31153.1; -.
EMBL; AF346709; AAK31153.1; JOINED.
EMBL; AF346710; AAK31153.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000276; GPCR_Rhodpsn
InterPro; IPR002131: Gnhrmn
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InterPro; IPR003591; IRR typ.
Pfam; PR00001; 7tm 1.
Pfam; PR00560; IRR; 15.
Pfam; PR01462; IRRNT; 1.
        protein-coupled receptor 48)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF257182; AAF68989.1;
HSSP; Q9BZR6; 10ZN.
Genew; HGNC:13299; GPR48.
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                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                               KDIMKNGKSNHLKQFRVAALLAFLGATVAGCFPLFHRGEYSASPLCLPFPTGETPSLGFT 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00013; LRRAT; 1.
SMART; SM0369; LRR TYP; 5.
PROSITE; PS0237; G_PROTEIN RECEP_F1_1; FALSE_NEG.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Leucine-rich repeat; Repeat; Signal; Transmembrane.
                                                                                                                                        FSSLINLTFISPEVIKFILLVVVPLPACLNPLLYILFNPHFKEDLVSLRKQTYVWTRSKH
                           KYSAKPETKAPFSSLKVIILLCALLALTMAAVPLLGGSKYGASPLCLPLPFGEPSTMGYM
                                                                                                             VALILLNSLCFLMMTIAYTKLYCNLDKGDLENIWDCSMVKHIALLLFTNCILNCPVAFLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leucine-rich repeat-containing G protein-coupled receptor 4 precursor
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: Orphan receptor.
-i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
-i- SIMILARITY: Contains 15 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hsu S.Y., Liang S.-G., Hsueh A.J.W.;
"Characterization of two LGR genes homologous to gonadotropin and
thyrotropin receptors with extracellular leucine-rich repeats and
protein-coupled, seven-transmembrane region.";
Mol. Endocrinol. 12:1830-1845(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99065210; PubMed=9849958; DOI=10.1210/me.12.12.1830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 41, Last sequence update) (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                              951 AA
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InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003591; LRR_typ.
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InterPro; IPR002131; Gphrmn_recept
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PRINTS; PR00237; GPCRRHODOPSN
PRINTS; PR00019; LEURICHRPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Gpr48; Synonyms=Lgr4;
Rattus norvegicus (Rat).
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Pfam; PF00560; LRR; 15.
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SVSVSISS 832
                                                                                                                                                                                                                                                                                          PSLMSINS 854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 YLDLSMNNISQLLPNPLPSLRFLEELRLAGNALTYIPKGAFTGLYSLKVLMLQNNQLRHV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> S (in Ref. 1; AAF68989)
-> P (in Ref. 1; AAF68989)
-> S (in Ref. 1; AAF68989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 50.7%; Pred. No. 2.9e-116;
Matches 430; Conservative 124; Mismatches 271; Indels
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LRR 1.

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LRR 3.

LRR 4.

LRR 5.

LRR 6.

LRR 7.

LRR 8.

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LRR 10.

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LRR 13.

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LRR 16.

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50.7%; Pred. No. 2.9e-116;
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Best Local Similarity
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MEDINE-223825; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE-223825; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heiseh F.,

Bransten M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

A Richards S., Worley K.C., Hale S.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Rodenezation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                           TGILTFLDAVSWGRFAEFGIWWETGSGCKVAGSLAVFSSESAVFLLTLAAVERSVFAKDL 650
                                                PCEXLLGSWMIRLTWWFIFLVALLFNLLVILTVPASCSSLPASKLFIGLISVSNLLMGIY
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                                                                                                              KISNOWNKGDNSSMDDLHKKDAGMFQAQDERDLEDFLLDFEEDLKALHSVQCSPSPGPFK
                                                                                                                                         AKFETKAPFSSLKVI ILLCALLALTMAAVPLLGGSKYGASPLCLPLPFGEPSTMGYMVAL
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Last sequence update)
Last annotation update)
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01-OCT-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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Homo sapiens (Human)
Eukaryota, Metazoa,
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SVSISS 832
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TISSUE=Brain;
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coupled receptor 4.
Extracellular (Potential).
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                                                                                                            Cytoplasmic (Forential).
2 (Potential).
Extracellular (Potential).
3 (Potential).
Cytoplasmic (Potential).
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Extracellular (Potential)
5 (Potential).
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Extracellular (Potential)
7 (Potential).
Cytoplasmic (Potential).
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LRR 3.

LRR 4.

LRR 5.

LRR 6.

LRR 7.

LRR 8.

LRR 9.

LRR 10.

LRR 11.

LRR 11.

LRR 13.

LRR 13.

LRR 14.

LRR 14.

LRR 14.

LRR 15.

LRR 16.

LRR 16.

LRR 17.

LRR 17.

LRR 18.

LRR 18.

LRR 19.

LRR 19.

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LRR 10.

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GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016500; P:protein-hormone receptor activity; IEA.

GO; GO:007186; P:G-protein coupled receptor protein signalin.

InterPro; IPR002731; GPCR Modpan.

InterPro; IPR001311; Gphrm. receptor.

InterPro; IPR001611; LRR.

InterPro; IPR001611; LRR.

InterPro; IPR001891; IRR.

InterPro; IRR.

InterPro; IRR.

InterPro; IRR.

InterPro; IPR001891; IRR.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 43.1%; Score 2024.5; DB 2; Length Best Local Similarity 49.2%; Pred. No. 2.8e-112; Matches 420; Conservative 125; Mismatches 254; Indels
                                          the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO037; GLYCHORMONER.
PRINTS; PRO0237; GPCREHODDEN.
PRINTS; PRO0137; LEURICHRFT.
SWART; SMO019; LERR TYP; 5.
PROSITE; PSSO262; GPROTEIN RECEP F1_2; 1.
PROSITE; PSSO262; GINC FINER CHART.
SROGOSE; ZINC FINER CHART.
SROGUSER; ZINC FINER CHART.
SROGUSER; ZINC FINER CHART.
SROUGHNCE 927 AA; 101676 MW; C7B2F0C40ES84GE8 CRC64;
Strausberg R.; Submitted (JJN-2002) to the EMBL; BC033039; AAH33039.1; EMBL; BC3147; 1D0B.
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Charles, College Managai E., Sugiyama T., Irie R., Makamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Nakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sakine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamanco J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y., Sudo H., Murakami K., Yawai T., Isono Y., Nakamura T., Ishii S., Najawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Sugawara M., Takahashi M., Katsuta N., Sato K., Tanikawa M., Waranaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Pujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S., Ono Y., Takiguchi S., Watanabe M., Haraoka S., Chiba Y., Rusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y., Matsunawa H., Satoh N., Jakani S., Ono Y., Takiguchi S., Matanabe M., Sasaki N., Aottuka S., Nomiyama H., Satoh N., Takani S., Tarashima Y., Suzuki O., Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe T., Kumagai A., Itakura S., Fukuzumi Y., Amagama K., Fujii Y., Cazaki K., Hirao M., Ohmori Y., Rawakami B., Amabata A., Hikhiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Kawabata A., Hikhiji T., Robatake N., Itakama Y., Shigeta K., Senba T., Kawabami T., Shigeta K., Shigeta K., Senba T.,
                                                                   ERSLSAKDIMKNGKSNHLKQFRVAALLAFLGATVAGCFPIFHRGEYSASPLCLPFPTGET
                                                                                                                                                 STMGYMVALILLNSLCFLAMMTIAYTKLYCNLDKGDLENIWDCSMVKHIALLLFTNCILNC
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ERGFSVKYSAKFETKAPFSSLKVIILLCALLALTMAAVPLLGGSKYGASPLCLPLPFGEP
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MEDIINE=22040266; PubMed=12044878; DOI=10.1016/S0014-5793(02)02775-8;
Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
"Identification of G protein-coupled receptor genes from the human genome sequence.";
FEBS Lett. 520:97-101(2002).
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Q9HBX8; Q6KK69;
28-FRB-2003 (Rel. 41, Created)
28-FRB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Leucine_rich repeat-containing G protein-coupled receptor
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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PubMed=14702039; DOI=10.1038/ng1285;
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Homo sapiens (Human).
---- Metazoa; Chordata;
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ID LGR6 HUMAN

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                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PRINTS; PRO0373; GLYCHORMORE.

PRINTS; PRO037; GPCRHHODOPEN.

PRINTS; PRO019; LEURICHRPT.

PROSITE; PSO0237; G PROTEIN RECEP F1 1; FALSE NEG.

PROSITE; PSSO262; G PROTEIN RECEP F1 2; FALSE NEG.

G-protein coupled receptor; Glycoprotein; Leucine-rich repeat; Repeat;

Transmembrane.
Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizushiima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura Y., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.; "Complete sequencing and characterization of 21,243 full-length human
                                                                           Nat. Genet. 36:40-45(2004).
-!- FUNCTION: Orphan receptor.
-!- SUBCELLUIAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
-!- SIMILARITY: Contains 11 leucine-rich (LRR) repeats.
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LERR 2.

LERR 3.

LERR 4.

LERR 5.

LER 6.

LERR 9.

LERR 9.

LERR 11.

LERR 11.

LERR 11.

N-linked (GlCNAC. ..) (Potential).

N-linked (GlCNAC. ..) (Potential).

N-linked (GlCNAC. ..) (Potential).

N-linked (HECRAC. ..) (Potential).
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Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential).
3 (Potential).
Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential).
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Extracellular (Potential).
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InterPro; IPR002131; Gphrmn_receptor.
InterPro; IPR001611; LRR.
InterPro; IPR003591; LRR_typ.
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EMBL; AB083616; BAB89329.1; -.
EMBL; AK027377; BAB55071.1; ALT_INIT.
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carminci P., Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W., Hukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hayashida K., Ishii Y., Itoh M., Kagawa I., Kanda M., Kando H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Nishi K., Nomura K., Shinagawa A., Shiraki T., Sagabe Y., Tagami M., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tomaru A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Bubilla Akolashizaki Y.;
Bubmitted (JUL-2001) to the EMBL/Genbank/DDBJ databasee.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/G1 TISSUE=Retina;
STRAIN=C57BL/G1 TISSUE=Retina;
STRAIN=C57BL/G21 TISSUE=Retina;
SEDIINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Mormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN=CS7BL/6J; TISSUE-Retina;
STRAIN=C9913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=2059031; PubMed=11076861; DOI=10.1101/gr.152600;
A MEDLINE=2059031; PubMed=11076861; DOI=10.1101/gr.152600;
A Konno H., Akiyama K., Nagaoka S., Sasaki N., Carninci P., Konno H., Ishiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Makamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., A Yoneda Y., Ishikawa T., Ozawa Y., Tanaka T., Matsuura S., Kawai J., A Okazaki Y., Muramatuu M., Inoue Y., Kira A., Hayashizaki Y.;
TRIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                          ij
                                                                                                                                                           STRAIN=C57BL/6J; TISSUE=Retina; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Mitgh-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=CSTBALF,61; TISSUE=Retina;
STRAIN=CSTBALO
THE FANTOM CONSORTIUM,
THE RIKEN GENOME Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation
Nature 420:563-673 (2002).
 18 musculus adult retina cDNA, RIKEN full-length enriched library,
lone:A930009A08 product:G PROTEIN-COUPLED RECEPTOR LGRA homolog
                                                            Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=C27BL/6J; TISSUE=Retina;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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GO:0016021; C:integral to membrane; IEA.
GO:0016500; F:protein-hormone receptor activity; IEA.
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                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                             NCBI_TaxID=10090;
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R GO; GO:0004872; F:receptor activity; IEA.

R GO; GO:0007186; P:G-protein coupled receptor protein signalin. ..;

R InterPro; IPR000213; GPRT Rhodpsn.

R InterPro; IPR00181; GPRT Rhodpsn.

R InterPro; IPR00181; GPRT R.

R InterPro; IPR00181; GPRT R.

R InterPro; IPR00181; IAR L.

R Ffam; PF00001; 7tm 1; 1.

R PFam; PF00001; 7tm 1; 1.

R PRINTS; PR00137; GPCRRHODOPSN.

R PRINTS; PR0019; LEURICHRPT.

R PRNAT; SM0019; LEURICHRPT.

R SMART; SM0019; LER TYP; 5.

R PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duery Match 41.3%; Score 1942.5; DB 2; Length 878; Best Local Similarity 52.3%; Pred. No. 2e-107; Atches 402; Conservative 112; Mismatches 233; Indels 21;
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The FANTOM CONSORTIUM, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002). STRAIN-C57BL/6J; TISSUE-Head; MEDLINE=20499374; Pubmd=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000). 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
library, clone:Cl30018C02 product:G protein-coupled receptor 49, full
insert sequence. SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE-Head;
Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Alzawa K., Akimura T., Hara A., Hashizume W., Hayashida S., Furuno M., Hanacto K., Hiraoka T., Hirozane T., Hori E., Imotrani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Hori F., Imotrani K., Ishii Y., Kondo S., Konno H., Kawai J., Kojima Y., Kondo S., Konno H., Kawai J., Kojima T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., STRAIN=C57BL/6J; TISSUE=Head; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; MEDLINE-2050013; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamotco R., Matsumoto H., Sakaguchi S., Ikegami T., Kabliwagi K., Fujiwake S., Inoue K., Togawa M., Ohara E., Watshiwagi K., Fujiwake S., Inoue K., Tozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rikik lintegrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001). FFPLPACLNPVLYVFFNPKFKDDWKLLKRRV---TR-KHGSVSVSISS 759 SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=Head; MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500; RIKEN FANYOM CONSORTHUM; Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999). Z 363 PRT; SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=Head; PRELIMINARY; SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. Name=Gpr49 716 Q8C8A7 RESULT 11 Q8C8A7 셤

360 61 PSNLSVFTSYLDLSMNNISQLPASIJHRLCFLEXLRLAGNALTHIFKGAFTGLHSLKVLM 120 240 240 300 301 FOHLPELRILTINGASHITEFPHLIGTATLESLTLIGAKISSLPQAVCDQLPNLQVLCVS 360 PSNLSVFTSYLDLSMANISQLLPNPLPSLRFLEELRLAGNALTYIPKGAFTGLYSLKVLM 120 LONNOLRHVPTEALONLRSLOSIRLDANHISYVPPSCFSGLHSLRHLWLDDNALTEIPVQ 180 180 9 9 Ξ. 181 AFRSLSALQAMTLALNKIHHIPDYAFGNLSSLVVLHLHNNRIHSLGKKCFDGLHSLETLD AFRSLSALQAMTLALNKIHHIADYAFGNLSSLVVLHIHNNRIHSLGKKCFDGLHSLETLD 241 LNYNNLDEFPTAIRTLSNLKELGFHSNNIRSIPEKAFVGNPSLITIHFYDNPIQFVGRSA FOHLPELRILILNGASQITEFPDLIGTANLESLILITGAQISSLPQTVCNQLPNLQVLDLS 1 MDTSRLGVILSLPVLLQLATGGSSPRSGVLLRGCPTHCHCEPDGRMILRVDCSDLGLSEL Gaps Herpin A., Favrel P., Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity)
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors. Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibatea K., Shibatea K., Shinadawa A., Shiraki T., Sogabe Y., Tagami Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2010) to the EMBL/GenBank/DDBJ databases. EMBL; AK04787; BAC33180.1; -- HSSP; QBER6; JOZN. Crassostrea gigas (Pacific oyster). Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Ostreoida; Ostreoidea; Ostreidae; Crassostrea. ., Length 363; 29; Indels 363 AA; 39879 MW; D5E2FC4449FCE2C0 CRC64; (TrEMBLrel. 27, Last sequence update) (TrEMBLrel. 27, Last annotation update) 34.2%; Score 1608; DB 2; 88.1%; Pred. No. 6.1e-88; live 14; Mismatches 29; MGD; MGI:1341817; Gpr49. GO; GO:0005615; C:extracellular space; TAS. GO; GO:0016021; C:integral to membrane; TAS. PRT; 1093 AA. (TrEMBLrel. 27, Created) Interpro; IPR00372; IRR_Nterm.
Interpro; IPR00372; IRR_Typ.
Pfam; PP01462; ILRRNT; 1.
Pfam; PF00560; ILR_1; 9.
PR.HYS; PR00101; ILRNTCHRPT.
SWART; SW00013; ILRNT; 1.
SWART; SW00369; ILRNT; 1. Glycoprotein hormone receptor. Best Local Similarity 88.18 Matches 317; Conservative InterPro; IPR001611; LRR PRELIMINARY; [1] SEQUENCE FROM N.A. 05-JUL-2004 (05-JUL-2004 (05-JUL-2004 (Name=gpr; SEQUENCE Query Match Best Local & 61 121 181 301 Receptor 26HA06; Q6HA06 RESULT 12 d ద a 셤 g δ g ઠ 8 Š ઠે 8

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Matches 284; Conservative 152;
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SEQUENCE FROM N.A.
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R GO; GO:0007186; P:G-protein coupled receptor protein signalin. .;

InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR001311; LRR.
InterPro; IPR001311; LRR.
InterPro; IPR003815; LRR cyst.
InterPro; IPR003815; LRR cyst.
InterPro; IPR003811; LRR_Verm.
INR PF000101; LRRNT; 1.
INR PRINTS; PR00137; GPCRANONER.
INR PRINTS; PR00137; GPCRANOPER.
INR SMART; SM00369; LRR_TYP; 14
INR SMART; SM0036
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                                      EPSTMGYMVALILLNSLCFLAMMTIAYTKLYCNLDKGDLENIWDCSMVKHIALLLFTNCIL
                                                                                                                                                                                                                                                                   NCPVAFLSFSSLINLTF1SPEVIKF1LLVVVPLPACLNPLLY1LFNPHFKEDLVSLRKQT
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EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL; AAABO1008964; EAA12259.2; -..

EMBL; AAABO1008964; EAA12259.2; -..

HSSP; P25147; 1D0B.

R GO; GO:0016500; P:protein-hormone receptor activity; IEA.

GO; GO:0016500; P:protein-hormone receptor protein signalin. .; I InterPro; IPR00121; GPCR_Rhodpsn.

InterPro; IPR00131; GPCR_Rhodpsn.

InterPro; IPR00151; LRR.

InterPro; IPR00151; LRR.

Pfam; PF00001; 7tm 1; 1.

R Pfam; PF00601; 7tm 1; 1.

R Pfam; PF00601; LRR_1; 16.
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Anophales gambiae str. PEST.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
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Pred. No. 1.5e-57;
!; Mismatches 394; Indels
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PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR0019; LEUNICHRPT.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
SEQUENCE 1257 AA; 139800 WW; 42C36285BD610A7B CRC64;
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Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 517 QDERDLEDFLLDFEEDLKALH-----SVQCSPSPGPFKPCEHLLDGWLIRIGVWTIA 568
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                                                               278 VGNPSLITIHFYDNPIQFVGRSAFQHLPELRTLTLNGASQITEFPDLTGTANLESLTLTG 337
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274 RRNQISEITSGALTNLTRLKVLDVDDNSLSSMPVGLENLMMLQEISASNNRIRWVSKGDF 333
                                                                                                  338 AQISSLPQTVCNQLPNLQVLDLSYNLLEDLPSFSVCQKLQKID-------
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                                                                                                                                                                                                                                                                                                                                       -----LRHNEIYEIKVDTFQQLLSLRSLNLAWNKIAIIHPNAFSTLPSLIKLDLSSNL
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CG8930-PA (CG8930-pb).
Name=rk; ORFNames=CG8930;
Drosophila melanogaster (Fruit fly)
Bukaryota; Merazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopteryota; Dibtera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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RA Man K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Gabor G.L.,
RA Ballew R.M., Bazandale J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Bazun A., Bazendale J., Bayraktarogolu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolahakov S.,
Berkon K.Y., Benos P.V., Berman B.P., Bhandari D., Botchan M.R., Bouck J., Broketein P., Brottier P.,
RA Gherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
Alalin M., Kaluuh P., Karpen G.H., Ke Z., Kennison J.A.,
Alalin M., Kaluuh P., Karpen G.H., Ke Z., Kennison J.R.,
Liu X., Mattei B., McIntcoh T.C., McLeod M.P., McPherson D.,
RA Harris W., Mattei B., McIntcoh T.C., McLeod M.P., McPherson D.L.,
RA Liu X., Mattei B., McIntcoh T.C., McLeod M.P., Morpherson D.L.,
RA Melson D.R., Nushon K., Nusekern D.R., Palazelo J.M.,
Ralasko P., Lei Y., Ranington K., Simpson M., Stupski M.P., Smith T.,
Shen K., Spadning A.A., Nixon K., Nusekern D.R., Palazelo J.M.,
Shier B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith T.,
RA Palazelo M., Pittman G.S., Pan S., D., Scheeler F., Shen H.,
RA Walliams S.M., Wowdagar T. Weinster E., Wang A.H., Wang X.,
RA Walliams S.M., Wowdagar W., Zhou K., Zho S., Zho 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
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SEQUENCE FROM N.A.

MEDLINE=22426065; PubMed=12537568;

MEDLINE=22426065; PubMed=12537568;

Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Laverty T., Wazny D.M., Nelson C.R., Recleb J.M., Park S., Pfeffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C. Weinstock G., Scherer S.E., Myers E.W., Glbbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: Release 3 of the Drosophila "Finishing a whole-genome shotgun: Release 3 of the Drosophila"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22426069; PubMed=12537572;
MiSIATE S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Mistas S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.,
Bettenrourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J. Kusso S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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FLSIFASESSVFLLTLAALERGFSVKYSAKFETKAPFSSLKVI ILLCALLALTMAAVPLL
                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
                                                                                                                                                                                                                                                                                                                                                           Glycoprotein hormone receptor II.
                                                                                                                                                                                                                     || :|: |
PPPLLPAAAVAHPPGC 1076
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PRINTS; PRO0327; GPCRHODOSEN.
PRINTS; PRO0019; LEWICHRPT.
SWART; SMO0369; LEWICHRPT.
                                                                                                                                                                                                      PPSSVPSPAYPVTESC 896
 642
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                                                                                                                                                                                                                                                                                                                                                                                                                        HVPTEALQNLRSLQSLRLDANHISYVPPSCFSGLHSLRHLWLDDNALTEIPVQAFRSLSA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                        |:|: | | : | | | : :|:|| | | : :|:|| | | : LEALNIGSNLLTIINDEDFPRMPNLIVLLLKRNQIMKISAGALKNLTALKVLELDDNLIS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSFSVCQKLQKIDLRHNEIYEIK-------VDTFQQLLSLRSL 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFPTAIRTLSNLKELGFHSNNIRSIPEKAFVGNPSLITIHFYDNPIQFVGRSAFQHLPEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                487 NAYKISNQ-----WNKGDNSSMDDLHKKDAG------MFQAQDERDLEDFLLDF---
                                                                                                                                                                                                                                                                                                                     QLAT-----GGSSPRSGVLLRGCPTHCHCRPDGRM-LLRVDCSDLGLSELPSNLSVF
                                                                                                                                                                                                                                                                                                                                                                       TSYLDLSMINISQLLPNPLPSLRFLEELRLAGNALTYIPKGAFTGLYSLKVLMLQNNQLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 SLPEGLSKLSQLQELSITSNRLRWINDTELPRSMQMLDMR--ANPLSTISPGAFRGMSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----EEDLKALHSVQCSPSPGPFKPCEHLLDGWLIRIGVWTIAVLALTCNALVTST
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                                                                                                                                                                                                                                                                                              Gaps
                  EMBL; AE003442; APF3347.3; — EMBL; AE00342; AFF3347.3; — EMBL; AE003542; AFF3347.3; — EMBL; AE003542; C:integral to membrane; IEA.
GO; GO:0016509; E:protein-horomone receptor activity; IEA.
GO; GO:0007186; E:G-protein coupled receptor protein signalin.
InterPro; IPR002376; GPCR_Rhodpsn.
InterPro; IPR001311; GPhrm. receptor.
InterPro; IPR003885; IRR Cyst.
InterPro; IPR003885; IRR Cyst.
FinterPro; IPR003891; LRR Cyst.
FinterPro; IPR003891; LRR Cyst.
FinterPro; IPR003891; IRR Cyst.
FinterPro; IPR003891; IRR Cyp.
                                                                                                                                                                                                                                                                                             118;
                                                                                                                                                                                                                                                                  22.8%; Score 1070; DB 2; Length 1360;
llarity 28.9%; Pred. No. 3.9e-55;
Conservative 153; Mismatches 423; Indels 118,
                                                                                                                                                                                                   SMART; SM03365; LRR SD22; 7.
SMART; SM00369; LRR TYP; 14.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SEQUENCE 1360 AA; 150772 WW; EBESBC47C933CD20 CRC64;
           the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   464 NFPELKVIEMPYAYQCCAP-----
                                                                                                                                                               PRINTS; PR00373; GLYCHORMONER.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR00019; LEURICHRPT.
                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                           282;
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68 TSYLDLSMNNISQLLPNPLPSLRFLEELRLAGNALTYIPKGAFTGLYSLKVLMLQNNQLR 127
GGSKYGASPLCLPLPFGE-PSTMGYMVALILLNSLCFLMMTIAYTKLYCNLDKGDLENIW
                                                                                                                                                                                                       DCSMVKHIALLLFTNCILNCPVAFLSFSSLINLTFISPEVIKFILLVVVPLPACLNPLLY
                                                                                                                                                                                                                                                                                                                              821 ILFNPHFKEDLVSLRKQTYVWTRSKHPSLMSINSDDVEKQSCDSTQALVTFTSSSITYDL
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STRAIN=Canton S.; TISSUE-Whole animal;
STRAIN=Canton S.; TISSUE-Whole animal;
STRAIN=Canton S.; TISSUE-Whole animal;
MEDLINE=20159836; PubMed=10899142; DOI=10.1101/gr.10.7.924;
Exiksen K.K., Hauser F., Schiott M., Pedersen K.-M., Soendergaard I Grimmelikhuijzen C.J.P.;
"Molecular cloning, genomic organization, developmental regulation, and a knock-out mutant of a novel leu-rich repeats-containing G protein-coupled receptor (DiGR-2) from Drosophila melanogaster.";
Genome Res. 10:924-938(2000).
EMBL, ARF66608.1; -.
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Bukaryota, Merazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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PlyBase; FBGN0003255; rk.
G0; G0:007564; P:regulation of cuticle tanning; IMP.
InterPro; IPR00275; GPCR Rhodpsn.
InterPro; IPR002131; Gphrmn_receptor.
InterPro; IPR001611; LRR.
InterPro; IPR001611; LRR.
InterPro; IPR001611; LRR.
IPR PR00101; 7tm 1; 1.
Pfam; PP00560; LRR 1; 16.
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Last annotation update)
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PS50262; G_PROTEIN_RECEP_F1_2; 1.
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1018 AIMTKQFKKDCVTL-----CKH----FEESRVVGGGGPGGRGAVARTKRG---DL 1060
                                                                                                                                       SLPEGISKLSQLQELSITSNRLRWINDTELPRSMQMLDMR--ANPLSTISAGAFRGMSKL 418
                                                                                                                                                                                                                                     DCSMVKHIALLFTNCILNCPVAFLSFSSLINLTFISPEVIKFILLVVVPLPACLNPLLY 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILFNPHFKEDLVSLRKQTYVWTRSKHPSLMSINSDDVEKQSCDSTQALVTFTSSSITYDL 880
181 VVVLDLGNNNLTKLEANSFFWAPNLEDLTLSDNSIINMDPNAFYGLAKLKRLSLQNCGLK 240
                                                                                      -----VDTFQQLLSLRSL 403
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                                              241 SLPPQSFQGLAQLTSLQLNGNALVSLDGDCLGHLQKLRTLRLEGNLFYRIPTNALAGLRT 300
                                                                        LOAMTLALNKIHHIPDYAFGNLSSLVVLHLHNNRIHSLGKKCFDGLHSLETLDLNYNNLD 247
                                                                                                                       248 EFPTAIRTLSNLKELGFHSNNIRSIPEKAFVGNPSLITIHFYDNPIQFVGRSAFQHLPEL 307
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Search completed: July 12, 2005, 07:36:34 Job time : 115 secs

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July 12, 2005, 07:34:32; Search time 614 Seconds (without alignments) 570.689 Million cell updates/sec
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1 MDTSRLGVLLSLPVLLQLAT......PAXPVTESCHLSSVAFVPCL 907
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Appl	Appl	App	App	App	App	l, Ap	Appl	App	App	App	
	16,	26,	264	422,	849	946	133	84,	158,	103	278	
Description	Sequence	Sequence						Seguence				
QI .	US-09-965-536A-16	US-09-970-944-26	US-10-251-385-264	US-10-225-567A-422	US-10-295-027-849	US-10-295-027-946	US-10-295-027-1331	US-10-751-736-84	US-10-482-029-158	US-10-505-486-103	US-10-251-385-278	
	10	10	14	14	15	15	15	16	11	11	14	
% Query Match Length DB	907	907	907	907	907	907	907	907	907	1145	907	
* Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	
Score	4702	4702	4702	4702	4702	4702	4702	4702	4702	4701	4696	
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DB 10; Length 907; Indels

100.0%; Score 4702; 100.0%; Pred. No. 0; tive 0; Mismatches

Query Match 100. Best Local Similarity 100. Matches 907; Conservative

TYPE: PRT ORGANISM: HUMAN US-09-965-536A-16

PRIOR APPLICATION NUMBER: 60/261,781
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/310,436
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 61
SEQ ID NO 16

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MDTSRLGVLLSLPVLLQLATGGSSPRSGVLLRGCPTHCHCEPDGRMLLRVDCSDLGLSEL
         MDTSRLGVILSLPVILQIATGGSSPRSGVILRGCPTHCHCEPDGRMILRVDCSDLGLSEL
                                                                 LONNOLRHVPTEALONLRSLOSLRLDANHISYVPPSCFSGLHSLRHLWLDDNALTEIPVO
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Sequence 26, Application US/09970944
Publication No. US20030204052A1
GENERAL INFORMATION:
APPLICANT: Harrman, John L
APPLICANT: Rastelli, Luca
APPLICANT: Shimkets, Richard A

RESULT 2 US-09-970-944-26

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TITLE OF INVENTION: No. US20030204052A1e1 Proteins and Nucleic Acids Encoding Same an TITLE OF INVENTION: Antibodies Directed Against these Proteins FILE REFERENCE: 21402-138
CURRENT APPLICATION NUMBER: US/09/970,944
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 60/237,862
PRIOR PLING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 26
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100.0%; Score 4702;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 907; Conservative 0; Mismatches
                                                                                                   TYPE: PRT
CRGANISM: Homo sapiens
US-09-970-944-26
                                                                                          LENGTH: 907
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Db 781 PVAFLSFSSLINLTFISPEVIKFILLVVVPLPACLNPLLYILFNPHFKEDLVSLRKQTYV 840	Db 481 AFGVCENAYKISNQWNKGDNSSMDDLHKKDAGMFQAQDERDLEDFLLDFEEDLKALHSVQ 540
QY 841 WTRSKHPSLMSINSDDVEKQSCDSTQALVIFISSSITYDLPPSSVPSPAYPUTESCHLSS 900 DD 841 WTRSKHPSLMSINSDDVEKQSCDSTQALVIFISSSITYDLPPSSVPSPAYPUTESCHLSS 900	Qy 541 CSPSPGPFKPCEHLLDGWLIRIGVWTIAVLALTCNALVTSTVFRSPLYISPIKLLIGVIA 600
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OY 901 VARVPCL 907	Qy 601 ANMMLIGYSSAVLAGYDAFTFGSFARHGAWWENVGCHYIGFLSIFASESSVFLLTLAAL 660
RESULT 3 US-10-251-385-264	QY 661 BRGFSVKYSAKFETKAPFSSLKVIILLCALLALTWAAVPLLGGSKYGASPLCLPLPFGEP 720
; Sequence 264, Application US/10251385 ; Publication No. US20030105292A1 ; Centent, INDODAMPTON.	CY 721 STWGYMVALILLANSLCFLAMTIAYTKLYCNLDKGDLENIWDCSMVKHIALLLFTNCILNC 780
, APPLICANT: Behan, Dominic P. ; APPLICANT: Chalmers, Derek T.	721 SIMGYMVALILLINSLCFLMMTIAYTKLYCNLDKGDLENIMDCSMVKHIALLLFTNCILNC
0030105292A1-Endogenous, Constitutively Activated 1-Coupled	Cy 781 PVAFLSFSSLINLTFISBEVIKFILLVVVPLPALINPLLYILFNPHFKEDLVSLKKOTYV 840 Human G
; FILE REPERENCE: AREN-0040 ; CURRENT APPLICATION NUMBER: US/10/251,385 ; CURRENT FILING DATE: 2002-09-20	QY 841 WTRSKHPSLANSINSDDVEKQSCDSTQALVTFTSSSITVDLPPSSVPSPAYPVTESCHLSS 900
LICATION NUME ING DATE: 199 SEQ ID NOS:	VAFVPCL
; SOTIMARE: FAURITH VEISION 3.1 ; SEQUENT: 907	DD SOI VARVECE SOI
; TYPE: PRT ; ORGANISM: Homo sapiens US-10-251-385-264	യഗ
Query Match 100.0%; Score 4702; DB 14; Length 907; Best Local Similarity 100.0%; Pred. No. 0; Matches 907; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	щО
TSRLGVLLSLPVLLQLATGGSSPRSGVLLRGCPTHCHCEPDGRMLLRVDCSDI 	
Qy 61 PSNLSVPTSYLDLSMNISQLLPNPLPSLRFLBELRLAGNALTYIPKGAFTGLYSLKVLM 120 Db 61 PSNLSVPTSYLDLSMNISQLLPNPLPSLRFLBELRLAGNALTYIPKGAFTGLYSLKVLM 120	; CURRENT APPLICATION NUMBER: US/10/225,567A ; CURRENT FILING DATE: 2001-12-19 ; PRIOR APPLICATION NUMBER: 6/257,144 ; PRIOR FILING DATE: 2000-12-19
OY 121 LQNNQLRHVPTEALQNLRSLQSLRLDANHISYVPPSCFSGLHSLRHMLDDNALTEIPVQ 180 121 LQNNQLRHVPTEALQNLRSLQSLRLDANHISYVPPSCFSGLHSLRHLMLDDNALTEIPVQ 180	Z O E
QY 181 AFRSLSALQAMTLALINKIHHIPDXAFGNLSSLVYLHLHDNRIHSLGKKCFDGLHSLETLD 240 DD 181 AFRSLSALQAMTLALINKIHHIPDXAFGNLSSLVYLHLHDNRIHSLIGKKCFDGLHSLETLD 240	; TYPE: PRT ; ORGANISM: Homo sapiens US-10-225-567A-422
241 LAYANLDEFPTAIRTLSNLKELGFHSNNIRSIPEKAFVGNPSLITIHFYDNPIQFVGRSA	Query Match 100.0%; Score 4702; DB 14; Length 907; Best Local Similarity 100.0%; Pred. No. 0; Matches 907; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DD 241 INTRNEDEFFIAIRTESNERELGFRSNNIRSIFERAFVGRFSLITHFIDNFIQFVGRSA 300 QY 301 FQHLPELRTLTLNGASQITEFPDLTGTANLESLTLTGAQISSLPQTVCNQLPNLQVLDLS 360 DA 301 FQHLPELRTLTLNGASQITEFPDLTGTANLESLTLTGAQISSLPQTVCNQLPNLQVLDLS 360 DA 301 FQHLPELRTLTLNGASQITEFPDLTGTANLESLTLTGAGISSLPQTVCNQLPNLQVLDLS 360	Oy 1 MDTSRLGVLLSLPVLLQLATGGSSPRSGVLLRGCPTHCHCEPDGRMLLRVDCSDLGLSEL 60
361 YNLLEDLESFSVCQKLQKIDLRHNEIVEIKVDTFQQLLSLRSLNLAWNKIAIIHPNAFST	Qy 61 PSNLSVFTSYLDLSMNNISQLLPNPLPSLRFLEELRLAGNALTYIPKGAFTGLYSLKVLM 120
421 LPGLIKLDLSSNLLSSPPITCLHGLTHLKLTGNHALQSLLSSRNSLNLAWNKLALIHFNAFST 421 LPGLIKLDLSSNLLSSPPITCLHGLTHLKLTGNHALQSLLSSENFPELKVIEMPYAYQCC	Cy 121 LONNOLRHVPTEALONIRSLOSLRLDANHISYVPPSCFSGLHSLRHLMLDDNALTEIPVO 180
DD 421 LPSLIKLDLSSNLLSSFPITGLHGLTHLKLTGNHALQSLISSENFPELKVIEMFYAYQCC 480 Qy 481 AFGVCENAYKISNQWNKGDNSSMDDLHKKDAGMFQAQDERDLEDFLEDFEEDLKALHSVQ 540	Cy 181 AFRSLSALQAMTLALNKIHHIDDYAFGNLSSLVVLHIHNNRIHSLGKKCFDGLHSLETLD 240

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61 PSNLSVFTSYLDLSMNNISQLEPNPLPSLRFLEELRLAGNALTYIPKGAFTGLYSLKVLM 120
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100.0%; Pred. No. 0;
ative 0; Mismatches
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-21
PRIOR FILING DATE: 2001-11-21
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-4
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR PHILOR DATE: 2002-01-08
PRIOR FILING DATE: 2002-01-09
PRIOR FILING DATE: 2002-01-01
PRIOR FILING DATE: 2002-01-01
PRIOR FILING DATE: 2002-01-01
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-03
PRIOR FILING DATE: 2002-02-13
PRIOR PRIOR PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
PRIOR PRIOR PRIOR APPLICATION NUMBER: US 60/356,714
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Matches 907; Conservative
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ORGANISM: Homo sapiens
US-10-295-027-849
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APPLICANT: Aziz, Natasha
APPLICANT: Aziz, Natasha
APPLICANT: Ginaberg, wendy M.
APPLICANT: Ginaberg, wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Heveri, Peter A.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Ess Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
CURRENT APPLICANION NUMBER: US/10/295,027
CURRENT PILING DATE: 2002-11-13
PRIOR PPLICATION NUMBER: US 09/663,733
PRIOR APPLICATION NUMBER: US 60/350,666
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Publication No. US20030232350A1
GENERAL INFORMATION:
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US-10-295-027-1331
; Sequence 1331, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
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 907; Conservative
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APPLICANT: AGEA: Daniel
APPLICANT: AGEA: Daniel
APPLICANT: AGEA: Daniel
APPLICANT: Ginberg, Wendy M.
APPLICANT: Marca, Peter A.
APPLICANT: Marcay, Richard
APPLICANTON NUMBER: US 60/350,666
PRIOR PILING DATE: 2001-11-13
PRIOR PLING DATE: 2001-11-12
PRIOR PLING DATE: 2001-11-12
PRIOR APPLICANTON NUMBER: US 60/332,464
PRIOR PLING DATE: 2001-11-12
PRIOR APPLICANTON NUMBER: US 60/340,376
PRIOR APPLICANTON NUMBER: US 60/347,211
PRIOR APPLICANTON NUMBER: US 60/347,211
PRIOR PLING DATE: 2001-12-14
PRIOR PLING DATE: 2001-20-1-10
PRIOR PLING DATE: 2002-01-10
PRIOR PLING DATE
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 946, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-10-295-027-946
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Best Local Similarity
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US-10-295-027-946
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APPLICANT: Wyeth
APPLICANT: Wattinez, Robert
APPLICANT: Brin, Biggine
APPLICANT: Liu, Wei, Biggine
APPLICANT: Liu, Wei, Biggine
APPLICANT: Liu, Wei, Biggine
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
FILE OF INVENTION: COMPOSITION COMPOSITIONS AND TREATING COLON
CURRENT APPLICATION NUMBER: US/10/751,736
FILE OF TILING DATE: 2003-01-06
PRIOR PRIOR FILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 54873
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361 YNLLEDLPSFSVCQKLQKIDLRHNEIYEIKVDTFQQLLSLRSLNLAWNKIAIIHPNAFST 420
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                                        421 LPSLIKLDLSSNLLSSFPITGLHGLTHLKLTGNHALQSLISSENFPELKVIEMPYAYQCC
                                                               481 AFGVCENAYKISNQWNKGDNSSMDDLHKKDAGMFQAQDERDLEDFLLDFEEDLKALHSVQ
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Best Local Similarity, 100.09
Matches 907; Conservative
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US-10-751-736-84
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                                                                     APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
TILLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and TILLE OF INVENTION: Methods of Exceening for Modulators of Cancer TILLE REFERENCE: 018501-012500US
CURRENT PLING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/335,464
PRIOR PRIOR DATE: 2001-11-21
PRIOR PLICK DATE: 2002-01-10
PRIOR PLICK DATE: 2002-01-13
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; Pred. No. 0;
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                                                         Glynne, Richard
Hevezi, Peter A.
Mack, David H.
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Best Local Similarity 100.
Matches 907; Conservative
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; ORGANISM: Homo sapiens
US-10-295-027-1331
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                                                Query Match 100.0%; Score 4702; Best Local Similarity 100.0%; Pred. No. 0; Matches 907; Conservative 0; Mismatches
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| Publication No. US20050037445A1
| GENERAL INFORMATION:
| TITLE OF INVENTION: Oncology drug innovation
| PILE REFERENCE: P 573 PC00
| CURRENT APPLICATION NUMBER: US/10/482,029
| CURRENT PILING DATE: 2003-12-29
| NUMBER OF SEQ ID NOS: 437
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 158
| LENGTH: 907
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Sequence 278, Application US/10251385
; Sequence 278, Application US/10251385
; Publication No. US20030105292A1
; GENERAL INFORMATION:
    APPLICANT: Behan, Dominic P.
    APPLICANT: Chalmers, Derek T.
    APPLICANT: Liaw, Chen W.
    TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G
    TITLE OF INVENTION: Protein-Compled
    TITLE OF INVENTION: Receptors
    TILE REFERENCE: AREN-0040
    TILE REFERENCE: AREN-0040
    CURRENT APPLICATION NUMBER: US/09/170,496
    PRIOR APPLICATION NUMBER: US/09/170,496
    PRIOR PILING DATE: 1998-10-13
    NUMBER OF SEQ ID NOS: 294
    SOFTWARE: Patentin version 3.1
    TUMBER OF SEQ ID NOS: 294
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Matches 906; Conservative
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; ORGANISM: Homo sapiens
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                           Sequence 103, Application US/10505486

Publication No. US20050118639A1

GENERAL INFORMATION:

APPLICANT: Takeda Chemical Industries, Ltd.

TITLE OF INVENTION:

CURRENT APPLICANTON NOBER: US/10/505,486

CURRENT APPLICATION NUMBER: US/10/505,486

CURRENT FILING DATE: 2004-08-20

PRIOR APPLICATION NUMBER: JP 2002-45728

PRIOR FILING DATE: 2002-02-23

PRIOR FILING DATE: 2002-03-33

PRIOR FILING DATE: 2002-07-23

PRIOR FILING DATE: 2002-07-23

PRIOR FILING DATE: 2002-07-23

PRIOR FILING DATE: 2002-07-23

PRIOR FILING DATE: 2002-10-11

NUMBER: OF SEQ ID NOS: 233

SEQ ID NO 103

LENGTH: 1145
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       Score 4701;
                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
99.9%; P
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Best Local Similarity 99.9
Matches 906; Conservative
                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Human
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US-10-505-486-103
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Db 361 YNLLEDLESFSVCQKLQKIDLRHNEIVEIKVDFFOOLLSLRSINLAMNKIAIIHPNAFST 420 421 LPGLIKLDLSSNLLSSFPITGLHGLTHLKLTGNHALQSLISSENFPELKVIEWFYAYQCC 480 421 LPGLIKLDLSSNLLSSFPITGLHGLTHLKLTGNHALQSLISSENFPELKVIEWFYAYQCC 480 481 AFGVCENAYKISNGNWCDNSSNDLHKCDGAPAQDEEDLEPPELDFEEDLKHISVQ 540 481 AFGVCENAYKISNGNWCDNSSNDDLHKCDGAPAQDEEDLEPPELDFEEDLKHISVQ 540 541 CSPSPGPFKPCEHLLDGMLIRIGWWTIAVTALTCNALYTSTPRSPLLIFEEDLKALHSVQ 540 541 CSPSPGPFKPCEHLLDGMLIRIGWWTIAVTALTCNALYTSTPRSPLLIFEEDLKALHSVQ 540 541 GSPSPGPFKPCEHLLDGMLIRIGWWTIAVTALTCNALYTSTPRSPLLIFEEDLKALHSVQ 540 601 AVMALTGVSSAVLAGVDAFPGSFARHGAWWENGYGCHVIGFLSIFASESSYFLLTLAAL 660 601 AVMALTGVSSAVLAGVDAFPGSFARHGAWWENGYGCHVIGFLSIFASESSYFLLTLAAL 660 601 AVMALTGVSSAVLAGVDAFPGSFARHGAWWENGYGCHVIGFLSIFASESSYFLLTLAAL 660 601 AVMALTGVSSAVLAGVDAFTGSFARHGAWWENGYGCHVIGFLSIFASESSYFLLTLAAL 660 601 AVMALTGVSSAVLAGVDAFTGSFARHGAWWENGYGCHVIGFLSIFASESSYFLLTLAAL 660 601 AVMALTGVSSAVLAGVDAFTGSFARHGAWWENGYGCHVIGFLSIFASESSYFLLTLAAL 660 602 AVMALTGVSSAVLAGVDAFTGSFARHGAWWENGYGCHVIGGSKYGASFLCLFDEFGBP 720 611 [

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TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and TITLE OP INVENTION: Methods of Screening for Modulators of Cancer, CURRENT APPLICATION NUMBER: 028501-012500US; CURRENT APPLICATION NUMBER: US 09/663,733 PRIOR PELICATION NUMBER: US 09/663,733 PRIOR PELICATION NUMBER: US 60/350,666 PRIOR FILING DATE: 2000-11-13 PRIOR PELICATION NUMBER: US 60/350,666 PRIOR FILING DATE: 2001-11-13 PRIOR PELICATION NUMBER: US 60/335,464 PRIOR PELICATION NUMBER: US 60/332,464 PRIOR PELICATION NUMBER: US 60/334,393 PRIOR PELICATION NUMBER: US 60/334,393 PRIOR PELICATION NUMBER: US 60/334,393 PRIOR PELICATION NUMBER: US 60/340,376 PRIOR PELICATION NUMBER: US 60/347,211 PRIOR PELICATION NUMBER: US 60/347,211 PRIOR PELICATION NUMBER: US 60/347,349 PRIOR PELICATION NUMBER: US 60/347,349 PRIOR PELICATION NUMBER: US 60/355,250 PRIOR PELICATION NUMBER: US 60/355,250 PRIOR PELICATION NUMBER: US 60/356,714 PRIOR PE
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Best Local Similarity 97.4%; Pred. No. 0;
Matches 883; Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
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US-10-295-027-484
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APPLICANT: Afar, Daniel

APPLICANT: Afar, Daniel

APPLICANT: Ginsberg, Wendy M.

APPLICANT: Ginsberg, Wendy M.

APPLICANT: Glyn, Kurt C.

APPLICANT: Glyn, Kurt C.

APPLICANT: Hevezi, Peter A.

APPLICANT: Marcal Bos bistechnology, Inc.

APPLICANT: Macon, Susan R.

APPLICANT: Watson, Susan R.

APPLICANT: Macon, Susan R.

APPLICANT: Bos Sidecechnology, Inc.

APPLICANT: Sold-11-13

FRIOR APPLICATION NUMBER: US 60/332,464

FRIOR FILING DATE: 2001-11-15

FRIOR PILING DATE: 2001-11-29

FRIOR PILING DATE: 2001-11-29

FRIOR PILING DATE: 2001-11-24

FRIOR APPLICATION NUMBER: US 60/347,211

FRIOR APPLICATION NUMBER: US 60/347,211

FRIOR APPLICATION NUMBER: US 60/347,211

FRIOR PILING DATE: 2002-01-10

FRIOR FILING DATE: 2002-01-10

FRIOR FILING DATE: 2002-01-10

FRIOR FILING DATE: 2002-01-10

FRIOR FILING DATE: 2002-02-13

FRIOR FILING DATE: 2002-02-13
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Publication No. US20030232350A1
GENERAL INFORMATION:
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RESULT 15

US-10-173-999-28

is Sequence 28, Application US/10173999

j Sequence 28, Application US/10173999

j Sequence 28, Application No. US2004000553A1

j GENERAL INFORMATION:

APPLICANT: Mack, David H.

APPLICANT: Gish, Kurt C.

APPLICANT: Gish, Kurt C.

APPLICANT: Gish, Kurt C.

APPLICANT: Gish, Kurt C.

TITLE OF INVENTION: and Methods of Diagnosis of Ovarian CITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian.

TITLE OF INVENTION: Cancer.

FILE REFERENCE: 018501-002420US

CURRENT FILING DATE: 2002-06-17

PRIOR APPLICATION NUMBER: US 60/299,234

PRIOR FILING DATE: 2001-06-18

PRIOR PILING DATE: 2001-08-27

PRIOR PILING DATE: 2001-08-27

PRIOR FILING DATE: 2001-04-12

PRIOR FILING DATE: 2001-04-12

NUMBER OF SEQ ID NOS: 163

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 28

LENGTH 883
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Best Local Similarity 97.4%;
Matches 883; Conservative
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US-10-173-999-28
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Best Local Similarity 97.4%;
Matches 883; Conservative
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US-10-295-027-1330
SEQ ID NO 1330
LENGTH: 883
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Gaps

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Scoring table:

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Ado29923 Human GPC
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Adr67869 Human HG3
Adn39567 Cancer/an
Adn39580 Cancer/an
Adn39580 Human HG3
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Aax23981 Human nete
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intracellular loop 3; transmembrane domain 6; drug screening; agonist;
antagonist; 88.
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      Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cog1_1/087PO spool/U310751736/runat_12072005_083640_22162/app_query.fasta_1.1095
-Q=/cog1_1/087PO spool/U310751736/runat_12072005_083640_22162/app_query.fasta_1.1095
-DB=N Geneseq_16Dec04 -QPMT=fastap -SUFFIX=oli.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
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-UST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=COTOR
-UST=45 -DOCALIGN=200 - THR_SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG -ICPU=3
-UND MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOPEXT=7
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Abz42816 Human G p
Adc22782 Human G p
Adh14255 Human HG3
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  (without alignments)
4689.262 Million cell updates/sec
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                       nucleic search, using frame_plus_p2n model
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Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical agents.

Example 1; Page 315-317; 341pp; English

The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743 and AAA30779-A30779). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, is substituted for an endogenous residue in IT63 at a position 16 amino acids N-terminal of an endogenous proline in TW6 to form a sequence X-CC (AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Pro may be endogenous, non-endogenous, or a mixture of endogenous and non-endogenous contains a protein of the properties of the profess of the pr antagonists, agonists and partial agonists for use as pharmaceutical agents. The mutant proteins are also useful in research settings for elucidating the roles of the receptors in normal and diseased conditions. Antagonists for a particular GPCR are useful for treating diseases and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous ligands. The present sequence represents cDNA encoding a human wild-type GPCR used in an exemplification of the invention. This was cloned and subjected to sitedirected mutagenesis (SDM) to generate DNA encoding the corresponding mutant of the invention

Sequence 2724 BP; 665 A; 723 C; 554 G; 782 T; 0 U; 0 Other;

LeuLeuProAsnProLeuProSerLeuArgPheLeuGluGluLeuArgLeuAlaGlyAsn 100 AlaLeuThrTyrIleProLysGlyAlaPheThrGlyLeuTyrSerLeuLysValLeuMet 120 GCTCTGACATACAFTCCCAAGGGAGCATTCACTGGCCTTTACAGTCTTAAAGTTCTTATG 360 CTGCAGAATAATCAGCTAAGACACGTACCCACAGAAGCTCTGCAGAATTTGCGAAGCCTT 420 121 GAGCCCGACGCAGGATGTTGCTCAGGGTGGACTGCTCCGACCTGGGGCTCTCGGAGCTG 180 crecrecceaarececrecearerecegerrecresassassiracererecesaase 300 LeuGlnAsnAsnGlnLeuArgHisValProThrGluAlaLeuGlnAsnLeuArgSerLeu 140 GlyGlySerSerProArgSerGlyValLeuLeuArgGlyCysProThrHisCysHisCys GluProAspGlyArgMetLeuLeuArgValAspCysSerAspLeuGlyLeuSerGluLeu MetAspThrSerArgLeuGlyValLeuLeuSerLeuProValLeuLeuGlnLeuAlaThr 1 Aragacacercegercegragererererererrecererererereradadere ProSerAsnLeuSerValPheThrSerTyrLeuAspLeuSerMetAsnAsnIleSerGln 2724 907 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: US-10-751-736-84 (1-907) x AAA30770 (1-2724) 0 907.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: Pred. No.: 241 21 61 41 61 81 101 301 121 à 셤 ò ద ò g ð g ò g ò 셤 ò

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		2521 IGGACAAGATCAAAAACACCCAAGCTTGATGATCAATTAACTCTGATGATGATGATGATGA 2580	q
GPCKs and antibodies are userul for diagnosing e treating immune-related diseases, growth-related regeneration-related disease. immunological-related		841 TrpThrArgSerLysHisProSerLeuMetSerlleAsnSerAspAspValGluLysGln 860	ò
antibody against a particular GPCR, and in the partibodies. The peptides and antibodies are also presence or absence of corresponding GPCRs. The		821 IleLeuPheAsnProHisPheLysGluAspLeuValSerLeuArgLysGlnThrTyrVal 840 	දු දු
protein-coupled receptor (GPCR) or a candidate pand (2) an isolated antibody having high specificavidity for a particular GPCR. (1) can be used a cene therapy. The anticenic peptides for GPCRs a		801 IleLysPheIleLeuLeuValValValProLeuProAlaCysLeuAsnProLeuLeuTyr 820 	දු පු
The present invention describes antigenic peptic any one of 1601 sequences (see ABP82019 to ABP83 acids. Also described: (1) an assay for the dete		781 ProvalataPheLeuserPheSerserleulleashLeunrheileserrogiuval 800 	B &
	X & :	. GACTGCTCTATGGTAAAACACATTGCCCTGTTGCTCTTCACCAACTGCATCCTAAACTGC	gg ,
	166	61 AspCysSerMetValLysHisIleAlaLeuLeuLheuPheThrAsnCysIleLeuAsnCys	<i>ह</i>
P-PSDB; ABP81968. New isolated antigenic peptides e.g., for G prot		741 ThrilealaTyrThrLysLeuTyrCysAsnLeuAspLysGlyAspLeuGluAsnIleTrp 760 	· 음 성
		2161 AGCACCATGGGCTACATGGTCGCTCTTGCTCATTTCCTTTGCTTCCTCATGATG 2220	e e
(LIFE-) LIFESPAN BIOSCIENCES INC. $\dot{\lambda}$	X & X	CIGGGIGGCAGCAAGIAIGGCGCCIC	a a
	XX	LeuGlyGlySerLysTyrGlyAlaSerProLeuCysLeuProLeuProPheGlyGluPro	à ·
(O)	<u> </u>	681 LeulysValileIleLeuLeuCysAlaLeuLeuAlaLeuThrMetAlaAlaValProLeu 700 	ራ የ
Homo sapiens.	×888	661 GluhrgGlyPheSerVallysTyrSerAlalysPheGluthrLysAlaProPheSerSer 680 	දු පු
psoriasis; anxiety; depression; schizophrenia; comental retardation; epilepsy; asthma; tuberculos hypertension; hypotension; renal disorder; rheur ulcer; gene; ds.	KW KW	GlyPheLeuSerIlePheAlaSerGluSerSerValPheLeuLeuThrLeuAlaAlaLeu 	දු දු
	*	621 PheGlySerPheAlaArgHisGlyAlaTrpTrpGluAsnGlyValGlyCysHisVallle 640 	දු පු
G protein-coupled receptor; GPCR; antigenic pept G protein-coupled receptor modulator; antibody;	X & & &	601 AlaValAsnMetLeuThrGlyValSerSerAlaValLeuAlaGlyValAspAlaPheThr 620 	දු දු
Human G protein-coupled receptor GPR49 nucleotic	B X 5	1741 ACAGTITICAGATCCCCCTCTGTACATTTCCCCCATTAAACTGTTAATTGGGGTCATCGCA 1800	qq
ABZ42816;	XX	ThrvalPheArgSerProLeuTyrlleSerProlleLysLeuLeulleGlyVallleAla	à
RESULT 2 ABZ42816 ID ABZ42816 standard; DNA; 2724 BP. XX	X	561 ArgileGlyValTrpThrileAlaValLeuAlaLeuThrCygAsnAlaLeuValThrSer 580 	<u>\$</u> 8
2701 GTGGCATTGCCATGTCTC 2721	중 음	541 CysSerProSerProGlyProPhelysProCysGluHisLeuLeuAspGlyTrpLeulle 560 	g &
2641 CCTCCCAGTTCCGTGCCATCAC	i 8 8	521 AspLeuGluAspPheLeuLeuAspPheGluGluAspLeuLysAlaLeuHisSerValGln 540 	6 G
2581 TCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGC	음 &		: 名
		501 SerSerMetAspAspLeuHisLysLysAspAlaGlyMetPheGlnAlaGlnAspGluArg 520	Š

JG 20 spent 2 10 cm Can Can pptide; gene therapy;
// immune-related disease;
// ited disease;
Ated disease;
Ated disease;
// osteoarthritis; allergy;
// rohn's disease; diabetes;
// multiple sclerosis; pain;
// dementia; memory loss;
// losis; obesity; nausea;
// nausea;
// nausea;
// osteoathritis; trauma; CTCCAGCATCACTTATGACCTG 2640 le SEQ ID NO:421.

lides (1) comprising: (a)
83519) of 12-24 amino
83519) of 12-24 amino
etection of a particular G
polypeptide in a sample;
fficity and high affinity or
as GPCR modulators and in
as GPCR modulators and in
as care useful in detecting an
production of specific
so useful for detecting the
e antigenic peptides for
and designing drugs for
ed diseases, cell
lated cell proliferative
or viral infections,
or viral infections,
opathy, chronic and acute

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inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42569 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention
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Sequence 2724 BP; 665 A; 723 C; 554 G; 782 T; 0 U; 0 Other;

		AlaThr 20 GCGACC 60	HisCys 40 CATTGC 120	9	GAGCTG 180 SerGln 80	 AGTCAG 240	GlyAsn 100	GGAAAC 300	12	CTTATG 360	14	AGCCTT 420	SerGly 160	AGTGGC 480	ValGln 180	Greeks 540	HisHis 200	CACCAC 600	AsnAsn 220	AACAAT 660	rLeuAsp 240	TTAGAT 720	LeuLys 260	CTTAAA 780
24		LeuLeuGlnLeuAl CTGCTGCAGCTGGC	ProThrHisCysH 	euGlyLeuSer	TGGGGCTCTCG etAsnAsnlle		euArgLeuAla	TACGICITGCG	erLeuLysVal	GTCTTAAAGTT	lnAsnLeuArg	AGAATTTGCGA	roSerCysPhe	CAAGCTGTTTC	hrGlullePro	CAGAAATCCC	euAsnLysile	TGAACAAAATA	euHisLeuHis	TACATCTCCAT	erLeuGluThr	GCCTAGAGACT	hrLeuSerAsn	CACTCTCCAAC
27 trive: 90 tes: 0		erLeuProVall 	albeubeuArgGlyCysP ngmgcngagggggcngcc	pCysSerAspt	CTGCTCCGACC		eLeuGluGluL	CCTGGAGGAGT	rGlyLeuTyrS	recertiaca	rGluAlaLeuG	AGAAGCTCTGC	rTyrvalProP	crarerecee	pAsnAlaLeuT	CAATGCGTTAA	tThrLeuAlaL	GACCTTGGCCC	rLeuValValL	crrecraerro	pGlyLeuHisS	TGGGCTCCACA	ralalleargT	TGCAATTAGGA
Length: Matches: Conservat Mismatche Indels:	(1-2724)	Valleuleuse GrGCrCcrGrC	erGlyValLeuLe creererect	LeuArgValAs	CTCAGGGTGGA ThrSerTyrLe		SerLeuArgPh	AGTCTCCGCTT	GlyAlaPheTh	GGAGCATTCAC	HisValProTh	caceraceae	AsnHisIleSe	AACCACATCAG	TrpLeuAspAs	recrecarea	LeuGlnAlaMe	TTGCAAGCCAT	AsnLeuSerSe	AACCTCTCCAG	LysCysPheAs	AAATGCTTTGA	GluPheProTh	GAATTCCCCAC
0 907.00 100.00\$ 100.00\$ 8	x ABZ42816	MetAspThrSerArgLeuGlyValLeuLeuSerLeuProValLeuLeuGlnLeuAlaTh 		GluProAspGlyArgMetLeuLeuArgValAspCysSerAspLeuGlyLeuSerGluLeu	GCAGGATGTTG euSerValPhe		LeuLeuProAsnProLeuProSerLeuArgPheLeuGluGluLeuArgLeuAlaGlyAsn	ATCCCCTGCCC	AlaLeuThrTyrileProLysGlyAlaPheThrGlyLeuTyrSerLeuLysValLeuMet	ACATTCCCAAG	euGlnAsnAsnGlnLeuArgHisValProThrGluAlaLeuGlnAsnLeuArgS	<u>ĊŢĠĊŔĠŔĂŢŔŔŢĊŔĠĊŢŔĠĠĊŖĊĠĊŖĊĠĊŖĠŖŖĠĊŢĠĊŖĠŖŔŢŢŢĠĊĠĸŖĠĊĊŢŢ</u>	GInSerLeuArgLeuAspAlaAsnHisIleSerTyrValProProSerCysPheSerGly	GTCTGGATGCT	LeuHisSerbeuArgHisLeuTrpLeuAspAspAsnAlaLeuThrGlu11eProValGln	TGAGGCACCTG	AlaPheArgSerLeuSerAlaLeuGlnAlaMetThrLeuAlaLeuAsnLysIleHisHis	GTTTATCGGCA	IleProAspTyrAlaPheGlyAsnLeuSerSerLeuValValLeuHisLeuHisAsnAsn	Argeertraga	ArglleHisSerLeuGlyLysLysCysPheAspGlyLeuHisSerLeuGluThrL	AGAATCCACTCCCTGGGAAAGAAATGCTTTGATGGGCTCCACAGCCTAGAGACTTTAGAT	LeuasnTyrasnasnLeuaspGluPheProThralalleargThrLeuSerasnLeulys	ATAACCTTGAT
s: ity: larity:	-84 (1-907)	MetaspThrS ATGGACACCT	GlyGlysers GGGGGCAGCT	GluProAspG 	GAGCCCGACG ProSerAsnL	CCTTCCAACC	LeuLeuProA	CTGCTCCCGA	AlaLeuThrT	GCTCTGACAT	LeuGlnAsnA	crecagaata	GlnSerLeuA	CAATCCCTGC	LeuHisSerL	CTGCATTCCC	AlaPheArgS	GCTTTTAGAA	IleProAspT	ATACCAGACT	ArglleHisS	AGAATCCACT	LeuAsnTyrA	TTAAATTACA
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The invention relates to a method for treating a non-endogenous, constitutively active version of an endogenous human G protein-coupled receptor (GPCR) that has a transmembrane-6 (TM6) region and an intracellular-3 (IC3) region, by substituting a specific amino acid in the TM6 region with a different amino acid, and testing for constitutive cutivity. The method is useful for creating a constitutively active version of an endogenous human GPCR that compounds for identification of region and an intracellular loop 3 region. The altered human GPCR copolypeptides are useful for screening test compounds for identification of inverse agonists or partial agonists of GPCR polypeptides, which may have therapeutic uses. The altered GPCRs may also be used in vivo or in vito in biological research. A nucleic acid encoding the altered GPCR vitro in biological research. A nucleic acid encoding the altered GPCR research a transgenic animal expressing the altered GPCR remay be used to create a transgenic animal expressing the altered GPCR. The method allows screening for compounds that modulate the activity of human G protein-coupied receptor without the head-for provision of a creening of compounds against orphan receptors for which no ligand is currently known. This sequence represents CDNA encoding a human GPCR contents.
                                                                                                                                                                                                                                                                                                                                                                Creating a constitutively active version of an endogenous human G protein coupled receptor (GPCR) comprises substituting a specific amino acid in the transmembrane-6 region with a different amino acid, and testing for
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   Homo sapiens
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PheGlySerPheAlaArgHisGlyAlaTrpTrpGluAsnGlyValGlyCysHisValIle
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                                                                       GlyPheLeuSerIlePheAlaSerGluSerSerValPheLeuLeuThrLeuAlaAlaLeu
                                                                                                                                             GluArgGlyPheSerValLysTyrSerAlaLysPheGluThrLysAlaProPheSerSer
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transmembrane-6 region; TM6; intracellular-3 region; IC3.
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ATCTTGTTCAATCCTCACTTTAAGGAGGATCTGGTGAGCCTGAGAAAGCAAACCTACGTC
                                                                                                                                                           TrpThrArgSerLysHisProSerLeuMetSerIleAsnSerAspAspValGluLysGln
                                                                                                                                                                                2521 TGGACAAGATCAAAACACCCAAGCTTGATGTCAATTAACTCTGATGATGTGGAAAAAAG
                                                                                                                                                                                                                                                                   TCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTATGACCTG
                                                                                                                                                                                                                                                                                                                      ProProSerSerVal ProSerProAlaTyrProValThrGluSerCysHisLeuSerSer
                                                                                                                                                                                                                                                                                                                                               CCTCCCAGTTCCGTGCCATCACCAGCTTATCCAGTGACTGAGAGCTGCCATCTTTCCTCT
                                                                                                                                                                                                                                          SerCysAspSerThrGlnAlaLeuValThrPheThrSerSerSerIleThrTyrAspLeu
                                                                             | IleLeuPheAsnProHisPheLysGluAspLeuValSerLeuArgLysGlnThrTyrVal
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98US-0095677P.
98US-00170496.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; non-endogenous; G
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P-PSDB; ADH14256.
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                                                                                                                                                                                                                                                               41 GluProAspGlyArgMetLeuLeuArgValAspCysSerAspLeuGlyLeuSerGluLeu
                                                                                                                                                                                                                                                                                 121 GAGCCCGACGCAGGATGTTGCTCAGGGTGGACTTGCTCCGACCTGGGGCTCTCGGAGGTG
                                                                                                                                                                                                                                                                                                                                  CTGCATTCCCTGAGGCACCTGTGGCTGGATGACAATGCGTTAACAGAAATCCCCGTCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    661 AGAATCCACTCCCTGGGAAAGAAATGCTTTGATGGGCTCCACAGGCTTTAGAT
                                                                                                                                                         MetAspThrSerArgLeuGlyValLeuLeuSerLeuProValLeuLeuGlnLeuAlaThr
                                                                                                                                                                                                                                                                                                                     ProSerAsnLeuSerValPheThrSerTyrLeuAspLeuSerMetAsnAsnIleSerGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 AlaPheArgSerLeuSerAlaLeuGlnAlaMetThrLeuAlaLeuAsnLysIleHisHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 IleProAspTyrAlaPheGlyAsnLeuSerSerLeuValValLeuHisLeuHisAsnAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             601 ATACCAGACTATGCCTTTGGAAACCTCTCCAGCTTGGTAGTTCTACATCTCCCATAACAAT
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Other;
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Db 1981 GAGCGTGGGTTCTCTGTGAATATTCTGCAAAATTTGAAACGAAAGCTCCATTTTCTAGC 2040	Oy 681 LeulysValileIleLeuLeuCysAlaLeuLeuAlaLeuThrMetAlaAlaValProLeu 700	Qy 701 LeuGlyGlySerLysflyAlaSerProLeuCysLeuProLeuProPheGlyGluPro 720	Oy 721 SerThrMetGlyTyrMetValAlaLeulleLeuLeuAsnSerLeuCysPheLeuMetMet 740	741 ThrilealaTyrThrLysLeuTyrCysAsnLeuAspLysGyAspLeuGluAsnIleTrp 		ProvalAlaPheLeuSerPheSerSerLeulleAsnLeuThrPhelleSerProGluVal 	801 IleLysPhelleLeuLeuValValValProLeuProAlacysLeuAnnProLeuLeuTyr 	Qy 821 IleLeuPheAanProfi.8PheLysGluAspLeuValSsrLeuArgLysGLnThriyrVal 840 	Oy 841 TrpThrArgSerLysHisProSerLeuMetSerIleAsnSerAspAspValGluLysGln 860	Oy 861 SerCygAspSerThrGlnAlaLeuValThrPheThrSerSerSerIleThrTyTASpLeu 880		Oy 901 ValAlaPheValProCysLeu 907 	3UL [32	AD132985; 22-APR-2004 (first entry)	DE Human G protein-coupled receptor (GPCR) 49 DNA. XX XX	XX OS Homo sapiens. XX XX US2003235910-A1.	XX PD 25-DEC-2003. XX DE 17_HTM_2002. 2003HG_00174456	17-JUN-2002; 2002US-0017445
301 PheGlnHisLeuProGluLeuArgThrLeuThrLeuAsnGlyAlaSerGln1leThrGlu 320 	PheProAspLeuThrGlyThrAlaAsnLeuGluSerLeuThrLeuThrGlyAlaGlnIle	Triccigatitaaciggaacigcaaccciggagagicigacitiaaciggagcacagaic SerSexLeuProGlnThrValCyaasnGlnLeuProAsnLeuGlnValLeuAspLeuSex 	CATCICITCCTCAAACCGTCTGCAATCACTTACCTAAATCTCCAAGTGCTAAAA yraanLeuLeuGluAspLeuProSerPheSerValCysGlnLysLeuGlnLyf 	LeuargiisasnGluileTyrGluileLysValaspThrPheGlnGlnLeuLeuSerLeu 	ArgSerLeuAsnLeuAlaTrpAsnLysIleAlaIleIleHisProAsnAlaPhe 	LeuProSerLeulleLysLeuAspLeuSerSerAsnLeuLeuSerSerPheProlleThr 	GlyLeuHisGlyLeuThrHisLeuLysLeuThrGlyAsnHisAlaLeuGlnSel 		81 AlaPheGlyValCygGluAsnAlaTyrLysIleSerAsnGlnTrpAsnLysGlyAspAsn 	SerSerMetAspaspLeuthisLysLysBaspalaGlyMetPheGlnAlaGluArg	AspleuGluAspPheLeuLeuAspPheGluGluAspLeuLysAlaLeuHisSerValGln	CysSerProSerProGlyProPheLysProCysGluHisLeuLeuAspGlyTrpLeuIle	ArgileGlyValTrpThrileAlaValLeuAlaLeuThrCysAshAlaLeuValThrSer 	581 ThrValPheArgSerProLeuTyrIleSerProlleLysLeuLeuIleGlyValIleAla 600 		621 PheGlySerPheAlaArgHisGlyAlaTrpTrpGluAsnGlyValGlyCysHisValIIle 640 	641 GlyPheLeuSerIlePheAlaSerGluSerSerValPheLeuLeuThrLeuAlaAlaLeu 660	

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The invention relates to a novel compound comprising a sequence targeted to a nucleic acid encoding G protein-coupled receptor (GPCR) 49, that specifically hybridises with the nucleic acid encoding G protein-coupled receptor 49 and inhibits its expression. The compound of the invention demonstrates neuroprotective activity and may be useful for preparing a composition for treating neural or endocrine system disorders, as well as during gene and antisense therapy. The current sequence is that of the human G protein-coupled receptor (GPCR) 49 DNA of the invention.
                                                                                                                                                        New antisense oligonucleotide comprising a sequence targeted to a nucleic acid encoding G protein-coupled receptor 49, useful for preparing a composition for treating e.g., neural or endocrine system disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2724 BP; 665 A; 723 C; 554 G; 782 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                   Example 13; SEQ ID NO 4; 60pp; English.
                       (ISIS-) ISIS PHARM INC.
                                                                Freier SM;
                                                                                                             WPI; 2004-070584/07.
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Alignment S. Pred. No.: Score: Percent Sim Best Local Query Match	t Scores: .: Similarity: al Similarity: tch:	0 907.00 100.00\$ 100.00\$ 12	Length: Matches: Conservative: Mismatches: Indels: Gaps:	2724 907 0 0 0	
US-10-751-736-84	136-84 (1-907)	x AD132985	(1-2724)		
λΌ	1 MetAspThrS	SerArgLeuGlyV	erArgLeuGlyValLeuLeuSerLeuProValLeuLeuGlnLeuAl	aThr	20
Db	1 ATGGACACC	TCCCGCTCGGTG	recrerererrecer		09
ò	21 GlyGlySer	SerProArgSerG	lyValLeuLeuArgGly	GlyGlySerSerProArgSerGlyValLeuLeuArgGlyCysProThrHisCysHisCys 4	40
qq	61 GGGGCAGC	TCTCCCAGGTCTG	GTGTGTTGCTGAGGGGC	GGGGGCAGCTCTCCCAGGTCTGGTGTGTGTGTGTGTGTGCTGCCCCCACACACA	120
à	41 GluProAsp	GlyArgMetLeuL	euArgValAspCysSer/	GluProAspGlyArgMetLeuLeuArgValAspCysSerAspLeuGlyLeuSerGluLeu 6	09
Db 1	121 GAGCCCGAC	GGCAGGATGTTGC	TCAGGGTGGACTGCTCC	GAGCCCGACGGCAGGATGTTGCTCAGGTGGACTGCTCCCGACCTGGGGCTCTCGGAGCTG 1	180
Š	61 ProSerAsn	LeuSerValPheT	hrSerTyrLeuAspLeu	ProSerAsnLeuSerValPheThrSerTyrLeuAspLeuSerMetAsnAsnIleSerGln 8	80
Db 1	181 CCTTCCAAC	CTCAGCGTCTTCA	CCTCCTACCTAGACCTC	CCTTCCAACCTCAGCGTCTTCACCTCCTAGCTCAGTCATGAACAACATCAGTCAG	240
ò	81 LeuLeuPro	AsnProLeuProS	erLeuArgPheLeuGlu(LeuLeuProAsnProLeuProSerLeuArgPheLeuGluGluLeuArgLeuAlaGlyAsn 10	100
Db 3	241 CTGCTCCCG	AATCCCTGCCCA	GTCTCCGCTTCCTGGAG	CTGCTCCCGAATCCCCTGCCCAGTCTCCTGGAGGAGTTACGTCTTGCGGGAAAC	300
ç.	101 AlaLeuThr	TyrlleProLysG	lyAlaPheThrGlyLeu	AlaLeuThrTyrIleProLysGlyAlaPheThrGlyLeuTyrSerLeuLysValLeuMet 1:	120
Dp 3	301 GCTCTGACA	TACATTCCCAAGG	GAGCATTCACTGGCCTT	GCTCTGACATACATTCCCAAGGAGCATTCACTGGCCTTTACAGTCTTAAAGTTCTTATG 3	360
ē	121 LeuGlnAsn	AsnGlnLeuArgH	isValProThrGluAla	LeuGlnAsnAsnGlnLeuArgHisValProThrGluAlaLeuGlnAsnLeuArgSerLeu 1.	140
Db 3	361 CTGCAGAAT	AATCAGCTAAGAC	ACGTACCCACAGAAGCT	CTGCAGAATAATCAGCTAAGACACGTACCCACAGAAGCTCTGCAGAATTTGCGAAGCCTT 4	420
9,	141 GlnSerLeu	ArgleuAspAlaA	snHislleSerTyrVall	GlnSerLeuArgLeuAspAlaAsnHis1leSerTyrValProProSerCysPheSerGly 1	160
Db 4	421 CAATCCCTG	CGTCTGGATGCTA	ACCACATCAGCTATGTG	CAATCCCTGCGTCTGGGTGCTAACCACATCAGCTATGTGCCCCCCAAGCTGTTTCAGTGGC 4	480
%	161 LeuHisSer	LeuArgHisLeuT	rpLeuAspAspAsnAlai	LeuHisSerLeuArgHisLeuTrpLeuAspAspAsnAlaLeuThrGluIleProValGln 1	180
do do	481 CTGCATTCC	CTGAGGCACCTGT	GGCTGGATGACAATGCG	CTGCATTCCCTGAGGCACCTGTGGCTGGATGACAATGCGTTAACAGAAATCCCCGTCCAG 5.	540
ç Ç	181 AlaPheArg	SerbeuSerAlab	euGlnAlaMetThrLeuJ	aPheArgSerLeuSerAlaLeuGlnAlaMetThrLeuAlaLeuAsnLysIleHisHis 2:	200
q ₀	541 GCTTTTAGA	AGTTTATCGGCAT	rgcaagccargaccrrg	GCTTTTAGAAGTTTATCGGCATTGCAAGCCATGACCTTGGCCCTGAACAAAATACACCAC 6	009

È	201	ValleuHisLeuHisAsnAsn 22
qq	601	ATACCAGACTATGCCTTTGGAAACCTCTCCAGCTTGGTAGTTCTACATCTCCATAACAAT 660
λ̈́o	221	ArgIleHisSerLeuGlyLysLysCysPheAspGlyLeuHisSerLeuGluThrLeuAsp 240
ДQ	661	AGAATCCACTCCCTGGGAAAGAAATGCTTTGATGGGCTCCACAGCCTAGAGACTTTAGAT 720
ò	241	LeuasnTyrasnasnLeuaspGluPheProThralalleArgThrLeuSerasnLeuLys 260
ф	721	TTAAATTACAATAACCTTGATGAATTCCCCACTGCAATTAGGACACTCTCCAACCTTAAA 780
ò	261	GluLeuGlyPheHisSerAsnAsnIleArgSerIleProGluLysAlaPheValGlyAsn 280
QQ	781	GAACTAGGATTTCATAGCAACAATATCAGGTCGATACCTGAGAAAGCATTTGTAGGCAAC 840
δ	281	ProSerLeulleThrIleHisPheTyrAspAsnProIleGlnPheValGlyArgSerAla 300
qq	841	CCTTCTTATTACAATACATTCTATGACAATCCCATCCAATTTGTTGGGAGATCTGCT 900
ò	301	2
ф	901	TTTCACATTTACCTGACTAAGAACACTGACTCTGAATGGTGCCTCACAAATAACTGAA 960
ζ	321	PheProAspLeuThrGlyThrAlaAsnLeuGluSerLeuThrLeuThrGlyAlaGlnIle 340
QQ	961	TITCCTGATTTAACTGGAACTGCAAACCTGGAGGTCTGACTTTAACTGGAGCACAGATC 1020
ò	341	SerSerLeuProGlnThrValCysAsnGlnLeuProAsnLeuGlnValLeuAspLeuSer 360
eg Q	1021	TCATCTTCCTCAAACCGTCTGCAATCAGTTACCTAATCTCCAAGTGCTAGATCTGTCT 1080
ò	361	TyrAsnLeuLeuGluAspLeuProSerPheSerValCysGlnLysLeuGlnLysIleAsp 380
qq	1081	TACAACCTATTAGAAGATTTACCCAGTTTTTCAGTCTGCCAAAAAGCTTCAGAAAATTGAC
Ġ	381	LeuArgHisAsnGluIleTyrGluIleLysValAspThrPheGlnGlnLeuLeuSerLeu 400
qq	1141	CTAAGACATAATGAAATCTACGAAATTAAAGTTGACACTTTCCAGCAGTGCTTAGCCTC 1200
ò	401	ArgSerLeuAsnLeuAlaTrpAsnLysIleAlaIleIleHisProAsnAlaPheSerThr 420
Dp	1201	CGATCGCTGAATTTGGCTTGGAAAAATTGCTATTATTCACCCCAATGCATTTTCCACT 1260
à	421	LeuProSerLeulleLysLeuAspLeuSerSerAsnLeuLeuSerSerPheProlleThr 440
Dp	1261	TIGCCATCCCTAATAAAGCTGGACCTATCGTCCACCTCTGTCGTCTTTTCCTATAACT 1320
č	441	GlyLeuHisGlyLeuThrHisLeuLySLeuThrGlyAsnHisAlaLeuGlnSerLeuIle 460
Dp	1321	GGGTTACATGGTTTAACTCACTTAAAATTAACAGGAAATCATGCCTTACAGAGCTTGATA 1380
ò	461	SerSerGluAsnPheProGluLeuLysValIleGluMetProTyrAlaTyrGlnCysCys 480
DÞ	1381	TCATCTGAAAACTTTCCAGAACTCAAGGTTATAGAAATGCCTTATGCTTACCAGTGCTGT 1440
à	481	AlaPheGlyValCysGluAsnAlaTyrLysIleSerAsnGlnTrpAsnLysGlyAspAsn 500
Ωp	1441	GCATTIGGAGIGIGAGAAIGCCIAIAAGAITICIAAICAAIGGAAIAAAGGIGACAAC 1500
ά	501	SerSerMetAspAspLeuHisLysLysAspAlaGlyMetPheGlnAlaGlnAspGluArg 520
QQ	1501	AGCAGTATGGACGACCTTCATAAGAAAGATGCTGGAATGTTTCAGGCTCAAGATGAACGT 1560
ò	521	AspleugluaspPheLeuLeuaspPheGlugluaspLeuLysAlaLeuHisSerValGln 540
qa	1561	16
\$	541	CysSerProSerProGlyProPheLysProCysGluHisLeuLeuAspGlyTrpLeuIle 560
οp	Ò	-63

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AD029923
ID AD029923 standard; CDNA; 2724 BP.

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AD029923;
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Eduna GPCR (first entry)
DE Human GPCR GPR49 polymuclectide, SEQ ID NO:1025.
XX
G protein-coupled receptor; GPCR; drug screening; diagnosis;
XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
XX G protein-coupled receptor; GPCR; drug screening; disorder;
XX Muscular disorder; luter disorder; immune disorder; breast disorder;
XX Muscular disorder; lung disorder; breast disorder;
XX Homo sapiens;
XX Homo sapiens.
XX Musculd: heptotropic; antiphroid; antialargic; anorectic;
XX Musculd: heptotropic; antiphroid; antiallergic; anorectic;
XX Musculd: heptotropic; duction therapy; GPCR modulator; human;
XX Musculd: heptotropic; duction therapy; defense therapy;
XX Musculd: heptotropic; duction therapy; duction therapy;

(PRIM-) PRIMAL INC.

Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F; Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H;

WPI; 2004-390329/36. P-PSDB; ADO29408. Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina pectoris, Parkinson's disease.

Claim 151; SEQ ID NO 1025; 542pp; English.

The invention relates to human and mouse G protein-coupled receptors (GPCRS) and nucleic acids encoding them. The invention also relates to sequences at least 9% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing and nucleic acids of the invention; methods of screening diseases compounds useful in the treatment of GPCR-related diseases; a transgenic compounds useful in the treatment of GPCR-related diseases; a transgenic compounds useful in the treatment of GPCR-related diseases; a transgenic computation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridise to GPCR polynucleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, comprisions) disease or schizophrenia); cliscates of the adrenal gland; disorders of the colon or intestine comprisions); disperies or the disconders of the calon and infarction); muscular disorders; blood disorders or anaemia or leukaemia); immune disorders; blood disorders or AIDS); bone and joint disorders (e.g., autoimmune disorders or AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid

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cc arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g., obesity, enzyme deficiency-related diseases or vitamin deficiency-related diseases); and disorders of the kidney, liver, lung, breast, ovary, ctrus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR-encoding cruclaic acid of the invention. Note: The full sequence data for this content did not form part of the printed specification; those sequences cont shown were obtained in electronic format directly from WIPO at Cfp. wipo.int/pub/published_pct_sequences.

ខ្ពង់ខ្ល	ftp.wipo Sequence	.int/pub/publ	ished_pct_se A; 723 C; 5	quences. 54 G; 782 T; 0 U	1, 0 Other;	
Aliga Pred Score Perce Best Query	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Duery Match:	res: arity: milarity:	7.00 0.00% 0.00%	Length: Matches: Conservative: Mismatches: Indels: Gaps:	2724 907 0 0 0	
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à	П		SerArgLeuGlyValL	euLeuSerLeuProV	MetAspThrSerArgLeuGlyValLeuLeuSerLeuProValLeuLeuGlnLeuAlaThr 20	
qq	г		TCCCGGCTCGGTGTGC	rccrerctreccre		
Š	21		SerProArgSerGlyV	AlleuleuArgGlyC	GlydlySerSerProArgSerGlyValLeuLeuArgGlyCysProThrHisCysHisCys 40	
gg	61		TCTCCCAGGTCTGGTG	TGTTGCTGAGGGGCT	GCCCCACACACTGTCATTGC 120	
Š	41		GlyArgMetLeuLeuA	rrgValAspCysSerA	GluProAspGlyArgMetLeuLeuArgValAspCysSerAspLeuGlyLeuSerGluLeu 60	
e G	121		GGCAGGATGTTGCTCA	GGGTGGACTGCTCCG	ACCTGGGGCTCTCGGAGCTG 180	
à	61		LeuSerValPheThrS	erTyrLeuAspLeuS	ProSerAsnLeuSerValPheThrSerTyrLeuAspLeuSerMetAsnAsnIleSerGln 80	
e G	181		CTCAGCGTCTTCACCT	CCTACCTAGACCTCA		
Š	81		AsnProLeuProSerL	euArgPheLeuGluG	LeuLeuProAsnProLeuProSerLeuArgPheLeuGluGluLeuArgLeuAlaGlyAsn 100	
a	241		AATCCCTGCCCAGTC	TCCGCTTCCTGGAGG	AGTTACGTCTTGCGGGAAAC 300	
à	101		TyrlleProLysGlyA	laPheThrGlyLeuT	AlaLeuThrTyr1leProLysGlyAlaPheThrGlyLeuTyrSerLeuLysValLeuMet 120	
g	301		TACATTCCCAAGGGAG	cattcactggccttt	ACAGTCTTAAAGTTCTTATG 360	
à	. 121		AsnGlnLeuArgHisV	alProThrGluAlaL	LeuGlnAsnAsnGlnLeuArgHisValProThrGluAlaLeuGlnAsnLeuArgSerLeu 140	
g	361		AATCAGCTAAGACACG	TACCCACAGAAGCTC	TGCAGAATTTGCGAAGCCTT 420	
à	141		ArgLeuAspAlaAsnH	[isIleSerTyrValP	GInSerLeuArgLeuAspAlaAsnHisIleSerTyrValProProSerCysPheSerGly 160	
셤	421		cercredarecraace	acarcagerargree	ccccaagcrerrrcagrege 480	
Š	161		LeudrgHisLeuTrpL	euAspAspAsnAlaL	LeuHisSerLeuArgHisLeuTrpLeuAspAsnAlaLeuThrGluIleProValGln 180	
a a	481		craaggaaccrarga	rggargacaargcgr	TAACAGAAATCCCGTCCAG 540	
Š	181		SerLeuSerAlaLeuG	lllllllllll	AlaPheArgSerLeuSerAlaLeuGlnAlaMetThrLeuAlaLeuAsnLysIleHisHis 200	
q	541		AGTTTATCGGCATTGC	AAGCCATGACCTTGG	ccrcaacaaaracaccac 600	
Š	201		TyrAlaPheGlyAsnL	euSerSerLeuValV	IleProAspTyrAlaPheGlyAsnLeuSerSerLeuValValLeuHisLeuHisAsnAsn 220	
a a	109		TATGCCTTTGGAAACC	TCTCCAGCTTGGTAG	TTCTACATCTCCATAACAAT 660	
Š	221		SerLeuGlyLysLysC	ysPheAspGlyLeuH	ArglleHisSerLeuGlyLysLysCysPhcAspGlyLeuHisSerLeuGluThrLeuAsp 240	
a	661		TCCCTGGGAAAGAAAT	crrrearescre	ACAGCCTAGAGACTTTAGAT 720	
ò	241		AsnAsnLeuAspGluP	heProThrAlalleA	LeudsnTyrdsnAsnLeudspGluPheProThrAlaileArgThrLeuSerAsnLeuLys 260	
В	721		AATAACCTTGATGAAT	rccccacrgcaarra	GGACACTCTCCAACCTTAAA 780	

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a & a	1681 581	AGATTGGAGTGTGTGTGTGTGTGTGTGTGTGTTGTTGTTG
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                                                                                                                       CTGAAAGTAATCATTTTGCTCTGTGCCCTGCTGGCCTTGACCATGGCCGCAGTTCCCCTG
                                                                                                                                                 LeuGlyGlySerLysTyrGlyAlaSerProLeuCysLeuProLeuProPheGlyGluPro
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             GlyPheLeuSerIlePheAlaSerGluSerSerValPheLeuLeuThrLeuAlaAlaLeu
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                                                                         GluArgGlyPheSerValLysTyrSerAlaLysPheGluThrLysAlaProPheSerSer
                                                                                          GAGCGTGCGTTCTCTGTGAATATTCTGCAAAATTTGAAACGAAAGCTCCATTTTCTAGC
                                                                                                              LeuLysValIleIleLeuLeuCysAlaLeuLeuAlaLeuThrMetAlaAlaValProLeu
                                                                                                                                                           CTGGGTGGCAGCAGCAATATGGCGCCTCCCCTCTGTGCCTTTTGCCTTTTGGGGAGCCC
                                                                                                                                                                                       SerThrMetGlyTyrMetValAlaLeuIleLeuLeuAsnSerLeuCysPheLeuMetMet
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                                                                                                                                                                                                                                                                                                                                       IlelysPheileLeuLeuValValValProLeuProAlaCysLeuAsnProLeuTyr
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whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention also relates to expression vectors and host cells comprising a nucleic acid of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention, antibodies which specifically bind a polypeptide of the invention, use of such antibodies for drug targeting; colypeptides and mucleic acids. The nucleic acids, polypeptides, antibodies and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal necessaries and nucleic acids and uterine fibroids. They may also be useful in wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in Finological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kaiz N, Ginsburg WM, Gish KC, Glynne R, Hevezi PA;
Murray R, Watson SR, Wilson KE, Zlotnik A;
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08-FBB-2002; 2002US-0355250P.
13-FBB-2002; 2002US-0356714P.
20-FBB-2002; 2002US-0359077P.
29-MAR-2002; 2002US-0368809P.
04-APR-2002; 2002US-0370110P.
                                                                                                                                                                                                                                                                                                                                                                                            2001US-0350666P.
2001US-0332464P.
2001US-0334393P.
2001US-0335394P.
2001US-0340376P.
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16-JUL-2002; 2002US-0396839P.
22-JUL-2002; 2002US-0397775P.
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08-JAN-2002;
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US-10-75 Qy	US-10-751-736-84 (1-907) x ADN39796 (1-2880) Qy 1 MetAspThrSerArgLeuGlyValLeuSerLeuProValLeuLeuGlnLeuAlaThr 20	음 장	1069 TCATCTTCCTCAAACCGTCTGCAATCAGTTACCTAATCTCCAAGTGCTAGATCTGTCT 1128 361 TyrAsnLeuLeuGluAspLeuProSerPheSerValCysGlnLysLeuGlnLysIleAsp 380
		අ දි	1129 TACAACCTATTAGAAGATTTACCCAGTTTTTTCAGTCTGCCAAAAGCTTCAGAAAATTGAC 1188
	21 GlyGlySerSerProArgSerGlyValLeuLeuArgGlyCy8ProThrHisCy8HisCy8 40	S 8	STANDARD CONTROLL CONTROL C
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,	CCTTCCAACCTCAGCGTCTTCACCTCCTACCTAGACCTCAGTATGAACAACATCAGTCAG	8 &	441 GlyLeuHisGlyLeuThrHisLeuLysLeuThrGlyAsnHisAlaLeuGlnSerLeuIle 460
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	CARLCCCIGGOTCIGGOTGCCACGICAGCIAIGGCCCCCCCCAGCIGIIICAGIGGCCGCACGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGG	<i>&</i> 8	521 AspteugluaspPheteuLeuAspPheGluGluaspLeuLysAlaLeuHisSerValGln 540
	SHIB 20	ζζ Op	541 CysSerProSerProGlyProPheLysProCysGluHisLeuLeuAspClyTrpLeuIle 560
	nAsn 	& a	561 ArglleGlyValTrpThrIleAlaValLeuAlaLeuThrCysAsnAlaLeuValThrSer 580
	CAAT 70 uAsp 24	& 43	581 ThrvalPheargSerProLeuTyrIleSerProlleLysLeuLeuIleGlyValIleAla 600
	AGARICCACICCCIGGGGRANGSANIGCIIIGAIGGGCICCACAGCCIAGAGACIIIAGAI 70 LeudanTyrasnasnLeudapGluPheProThralaileArgThrLeuSerAsnLeuLys 26	8 %	601 AlaValAsnWetLeuThrGlyValSerSerAlaValLeuAlaGlyValAspAlaPheThr 620
	GluLeuGlyPheHisSerAsnAsnIleArgSerIleProGluLysAlaPheValGlyAsn 28	ò 8	621 PheGlySerPheAlaArgHisGlyAlaTrpTrpGluAsnGlyValGlyCysHisVallle 640
	GAACTAGGATTTCATAGCAACAATATCAGGTCGATACCTGAGAAAGCATTTGTAGGCAAC 88 ProSerLeulleThrileHisPheTyrAspAsnProlleGlnPheValGlyArgSerAla 30	\$ a	641 GlyPheLeuSerIlePheAlaSerGluSerSerValPheLeuLeuThrLeuAlaAlaLeu 660
	CCTTCTTATTACAATACATTTCTATGACAATCCCATCCAATTTGTTGGGGGGATCTGCT 948 PheGlnHisLeuproGluLeuargThrLeuThrLeuAsnGlyAlaSerGlnIleThrGlu 320	& g	661 GluargGlyPheSerValLysFyrSerAlalysPheGluThrLysAlaProPheSerSer 680
	TTTCAACATTTACCTGAACTAAGAACACTGACTCTGAATGGTGCCTCACAAATAACTGAA 100 PheProAspLeuThrGlyThrAlaAsnLeuGluSerLeuThrLeuThrGlyAlaGlnIle 340	& 43	681 LeulysValllelleLeuLeuCysAlaLeuLeuAlaLeuThrMetAlaAlaValProLeu 700
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GACTGCTCTATGGTAAAACACATTGCCCTGTTGCTCTTCACCAACTGCATCCTAAACTGC
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The invention relates to a method of identifying a mammal that will respond therapeutically to a method of treating cancer by administering an epidermal growth factor receptor (EGFR) modulator by comparing the level of a biomarker in a mammal before and after exposure to an EGFR modulator. The method comprises: (a) measuring, in the mammal, the level of a least one biomarker identified in the specification; (b) exposing the mammal to the EGFR modulator; and (c) measuring in the mammal the level of the biomarker, where a difference in the level in step (c) compared to step (a) indicates that the mammal will respond therapeutically to the method of treating cancer. The method and biomarkers are useful for identifying a mammal that will respond therapeutically to a method of treating cancer by administering an epidemmal growth factor receptor (EGFR) modulator. This sequence corresponds to one of the biomarkers whose levels of gene expression is measured in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence encodes the human G protein-coupled receptor (GPCR) known as HG38. The HG38 protein and corresponding nucleic acid, may be used in the method of the invention for detecting colon or lung cancer. The first method involves performing an assay to determine the amount of HG38 in a sample of colon or lung tissue, and comparing the amount of protein to standard, thus detecting expression of protein in sample, where the differential expression of protein in sample, where the differential expression of protein in sample when compared with the standard is diagnostic of colon or lung cancer. The second method involves hybridizing a composition comprising the HG38 coding sequence, or its complement, and a labelling moiety, to nucleic acids of a sample of colon or lung tissue under conditions to form at least one hybridization complex, detecting hybridization complex formation, and comparing complex formation to a standard, where the comparison reflects differential expression of the polynucleotide in the sample relative to the standard and is diagnosis before the patient is symptomatic. Anti-method enables eathier diagnosis before the patient is symptomatic. Anti-method enables eathier diagnosis before the patient is symptomatic. Anti-method enables eathier diagnosis before the patient is symptomatic.
                                                                                           gene; human ; G protein-coupled receptor ; GPCR; HG38; colon ; lung
                                                                                                                                                                                                                                                                                                                                                                                        Detecting colon or lung cancer, by determining amount of protein in sample, comparing amount of protein to standard, and differential expression of protein in sample indicates colon or lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2973 BP; 157 A; 759 C; 607 G; 850 T; 0 U; 0 Other;
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18. .2741
/*tag= a
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BP.
ADR67869 standard; cDNA; 2973
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                                                                    Human HG38 coding sequence
                                              (first entry)
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                                                                                                                              Homo sapiens.
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                                              18-NOV-2004
                                                                                                                                                                                                                                                                                                                                 Lasek AW;
                       ADR67869
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978 TTTCCTGATTTAACTGGAACTGCAAACCTGGAGAGTCTGACTTTAACTGGAGCACAGATC 1037 137 100 240 300 PheGlnHisLeuProGluLeuArgThrLeuThrLeuAsnGlyAlaSerGlnIleThrGlu 320 PheProAspLeuThrGlyThrAlaAsnLeuGluSerLeuThrLeuThrGlyAlaGlnIle 340 SerSerLeuProGlnThrValCysAsnGlnLeuProAsnLeuGlnValLeuAspleuSer 360 381 LeuArgHisAsnGluIleTyrGluIleLysValAspThrPheGlnGlnLeuLeuSerLeu 400 257 317 AlaLeuThrTyrIleProLysGlyhlaPheThrGlyLeuTyrSerLeuLysValLeuMet 120 377 LeuGlnAsnAsnGlnLeuArgHisValProThrGluAlaLeuGlnAsnLeuArgSerLeu 140 437 160 497 LeuHisSerLeuArgHisLeuTrpLeuAspAspAspAlaLeuThrGluIleProValGln 180 557 200 617 220 677 737 | LeuksnTyrksnAsnLeukspGluPheProThrAlaIlekrgThrLeuSerksnLeuLys 260 280 9 80 CCTTCTCTTATTACAATACATTTCTATGACAATCCCATCCAATTTGTTGGGGGGATCTGCT 918 TTTCAACATTTACCTGAACTAAGAACACTGACTGCTCTGAATGGTGCCTCACAAATAACTGAA 1038 TCATCTCCTCAAACCGTCTGCAATCAGTTACCTAATCTCCCAAGTGCTAGATCTGTCT TyrAsnLeuLeuGluAspLeuProSerPheSerValCysGlnLysLeuGlnLysIleAsp GluProAspGlyArgMetLeuLeuArgValAspCysSerAspLeuGlyLeuSerGluLeu LeuLeuProAsnProLeuProSerLeuArgPheLeuGluGluLeuArgLeuAlaGlyAsn GCTCTGACATACATTCCCAAGGAGCATTCACTGGCCTTTACAGTCTTAAAGTTCTTATG CTGCATTCCCTGAGGCACCTGTGGCTGGATGACAATGCGTTAACAGAAATCCCCGTCCAG AlaPheArgSerLeuSerAlaLeuGlnAlaMetThrLeuAlaLeuAsnLysIleHisHis GCTTTTAGAAGTTTATCGGCATTGCAAGCCATGACCTTGGCCCTGAACAAATACACCAC ArgileHisSerLeuGlyLysLysCysPheAspGlyLeuHisSerLeuGluThrLeuAsp AGAATCCACCCCGGGGAAAGAAATGCTTTGATGGGCTCCACAGCCTAGAGATTTAGAT GluLeuGlyPheHisSerAsnAsnIleArgSerIleProGluLysAlaPheValGlyAsn ProSerLeulleThrlleHisPheTyrAspAsnProIleGlnPheValGlyArgSerAla ProSerAsnLeuSerValPheThrSerTyrLeuAspLeuSerMetAsnAsnIleSerGln GlnSerLeuArgLeuAspAlaAsnHis1leSerTyrValProProSerCysPheSerGly CAATCCCTGCGTCTGGATGCTAACCACATCAGCTATGTGCCCCCAAGCTGTTTCAGTGGC 361

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US-10-751-736-84 (1-907) x ADR67869

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The invention relates to nucleic acids and proteins (ADN19683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
other diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
patient by detecting a nucleic acid at least 80% identical to those of
the invention or by detecting a polypeptide of the invention. The
invention also relates to expression vectors and host cells comprising a
nucleic acid of the invention; use of such antibodies for drug targeting;
and methods of screening for modulators of activity or expression of the
polypeptides and mucleic acids. The nucleic acids, polypeptides,
antibodies and methods are useful for diagnosing, prognosing and treating
cancer and other conditions such as psoriasis, ischaemia, heart disease,
atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
neovascularistation syndromes, scarring and uterine fibroids. They may
also be useful in wound healing and in contraception. The present
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                                                                                                                                                                                                                                        Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence represents a nucleic acid sequence of the invention
                                                                                                                                     Gish KC, Glynne R, Hevezi
Wilson KE, Zlotnik A;
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                                                                                                                                     Aziz N, Ginsburg WM,
Murray R, Watson SR,
05-JUN-2002; 2002US-0386614P.
16-UUJ-2002; 2002US-039639P.
22-JUL-2002; 2002US-039775F.
22-JUL-2002; 2002US-0397845P.
09-SEP-2002; 2002US-0409450P.
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                                                                                                                                 CTGCATTCCCTGAGGCACCTGTGGCTGGATGACAATGCGTTAACAGAAATCCCCGTCCAG
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CTGCAGAATAATCAGCTAAGACACGTACCCACAGAAGCTCTGCAGAATTTGCGAAGCCTT
                                            GlnSerLeuArgLeuAspAlaAsnHisIleSerTyrValProProSerCysPheSerGly
                                                               AlaPheArgSerLeuSerAlaLeuGlnAlaMetThrLeuAlaLeuAsnLysIleHisHis
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                                                                                                                                                                                                                                                                                                                                                                          Human; differential expression; cancer; angiogenic disorder; fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
      TGGACAAGATCAAAACACCCAAGCTTGATGTCAATTAACTCTGATGTGATGTGAAAAACA
                                                               2841 CCTCCCAGTTCCGTGCCATCACCAGCTTATCCAGTGACTGAGAGGGGGCCCATCTTTCCTCT
                                                                                                      ProProSerSerVal ProSerProAlaTyrProValThrGluSerCysHisLeuSerSer
                                             SerCysAspSerThrGlnAlaLeuValThrPheThrSerSerIleThrTyrAspLeu
                                                                                                                                                                                                                                                                                                                                                Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:A130.
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Wilson KE, Zlotnik A;
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Murray R, Watson SR,
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21-NOV-2001; 2001US-0332464P.
23-NOV-2001; 2001US-03323439P.
03-DEC-2001; 2001US-0335394P.
14-DEC-2001; 2001US-0345394P.
10-JAN-2002; 2002US-034731P.
10-JAN-2002; 2002US-0347349P.
08-FEB-2002; 2002US-035550P.
13-FEB-2002; 2002US-0356907P.
29-MAR-2002; 2002US-0368809P.
04-APR-2002; 2002US-0368809P.
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05-JUN-2002; 2002US-0386614P.
16-JUL-2002; 2002US-0396839P.
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22-JUL-2002; 2002US-0397845P.
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2361 AGCACCATGGGCTACATGGTCGCTCTCATCTTGCTCAATTCCCTTTGCTTCCTCATGATG
                                                           SerSerMetAspAspLeuHisLysLysAspAlaGlyMetPheGlnAlaGlnAspGluArg
                                                                            AGCAGTATIGGACGACCTTCATAAGAAAGATGCTGGAATGTTTCAGGCTCAAGATGAACGT
                                                                                                                                                                                                                                                         PheGlySerPheAlaArgHisGlyAlaTrpTrpGluAsnGlyValGlyCysHisValIle
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                                                                                                                                                                                                                                                                                                                                                            AlaValAsnMetLeuThrGlyValSerSerAlaValLeuAlaGlyValAspAlaPheThr
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whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological call in a patient by detecting a mucleic acid at least 80% identical to those of the invention also relates to expression vectors and host cells comprising a nucleic acid of the invention, antibodies which specifically bind a polypeptide of the invention, antibodies which specifically bind a polypeptide of the invention, antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and mucleic acids. The nucleic acids, polypeptides, cancer and other conditions such as psoriasis, ischaemia, heart disease, attribodies and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, attributed and conditions such as psoriasis, ischaemia, heart disease, an encared conditions such as psoriasis, ischaemia, many also be useful in wound healing and in contraception. They may also be useful in wound healing and in contraception. They may also be useful in wound healing and in contraception. The present (ADN38683-ADN40064) proteins nucleic acids and t invention relates \$

Sequence 3032 BP; 729 A; 816 C; 648 G; 839 T; 0 U; 0 Other;

3032	907	0	0	0	0
Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
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US-10-751-736-84 (1-907) x ADN39530 (1-3032)

i i i i i i	-	MetAspThrSerArgLeuGlyValLeuLeuSerLeuProValLeuLeuGlnLeuAlaThr
qq	201	ATGGACACCTCCCGGCTCGGTGTGCTCCTGTCCTTGCCTGTGCTGCT
δ	21	GlyGlySerSerProArgSerGlyValLeuLeuArgGlyCysProThrHisCysHisCys 40
οg	261	GGGGGCAGCTCTCCCAGGTCTGGTGTTGCTGAGGGCCTGCCCCACACACTGTCATTGC 320
δ	41	GluProAspGlyArgMetLeuLeuArgValAspCysSerAspLeuGlyLeuSerGluLeu 60
QQ	321	GAGCCCGACGCAGGATGTTGCTCAGGTGGACTGCTCCCGACCTGGGGCTCTCGGAGCTG 380
ò	61	ProSerAsnLeuSerValPheThrSerTyrLeuAspLeuSerMetAsnAsnIleSerGln 80
qq	381	CCTTCCAACCTCAGCGTCTTCACCTCCTACCTCAGACCTCAGTATGAACAACATCAGTCAG
à	81	LeuLeuProAsnProLeuProSerLeuArgPheLeuGluGluLeuArgLeuAlaGlyAsn 100
qq	441	CIGCICCCGAATCCCCTGCCCAGTCTCCGCTTCCTGGAGGAGTTACGTCTTGCGGGAAAC 500
Š	101	AlaLeuThrTyrIleProLysGlyAlaPheThrGlyLeuTyrSerLeuLysValleuWet 120
Dp	501	GCTCTGACATACATTCCCAAGGGAGCATTCACTGGCCTTTACAGTCTTAAAGTTCTTATG 560
č	121	LeuGlnAsnAsnGlnLeuArgHisValProThrGluAlaLeuGlnAsnLeuArgSerLeu 140
qq	561	CTGCAGAATAATCAGCTAAGACACGTACCCACAGAAGCTCTGCAGAATTTGCGAAGCCTT 620
δ	141	GlnSerLeuArgLeuAspAlaAsnHisIleSerTyrValProProSerCysPheSerGly 160
qq	621	CAATCCCTGCGTCTGGATGCTAACCACATCAGCTATGTGCCCCCCAAGCTGTTTCAGTGGC 680
λõ	161	LeuHisSerLeuArgHisLeuTrpLeuAspAsnAlaLeuThrGluIleProValGln 180
qa	681	CTGCATTCCCTGAGGCACCTGTGGCTGGATGCGTTAACAGAAATCCCCGTCCAG 740
δ	181	AlaPheArgSerLeuSerAlaLeuGlnAlaMetThrLeuAlaLeuAsnLysIleHisHis 200
qa	741	GCTTTTAGAAGTTTATCGGCATTGCAAGCCATGACCTTGGCCCCTGAAAATACACCAC 800
ò	201	IleProAspTyrAlaPheGlyAsnLeuSerSerLeuValValLeuHisLeuHisAsnAsn 220

801	ATACCAGACTATGCCTTTGGAAACCTCTCCAGCTTGGTAGTTCTACATCTCCCATAACAAT 860
221	euasp 24 Tagar 92
	euasnTyrasnasnLeuaspGluPheProThralalleArgThrLeuSerAsnLeuLys 2
261	lleuGlypheHisSerAsnAsnIleArgSerIleProGluLysAlaPheValGlyAsn 28
281	.leullethrileHisPheTyrAspAsnProlleGlnPheValGlyArgSerAla 3
301	PheGlnisLeuProGluLeuArgThrLeuThrLeuAsnGlyAlaSerGlnIleThrGlu 320
321	PheProAspLeuThrGlyThrAlaAsnLeuGluSerLeuThrLeuThrGlyAlaGlnIle 340
341	SerSerLeuProGlnThrValCysAsnGlnLeuProAsnLeuGlnValLeuAspLeuSer 360
361	sp 38
381	eu 40
401	hr 42
421	hr 44
441	le 46
461	SerSerGluabnPheProGluLeuLysVall1leGluWetProTyrAlaTyrGlnCysCy8 480
481	AlaPheGlyValCysGluAsnalaTyrLysIleSerAsnGlnTrpAsnLysGlyAspAsn 500
501	ABDGluArg 52 SATGAACGT 17
521	udapleulysalaleunisservalgin 54º
541	CysSerProSerProGlyProPheLysProCysGlutisLeuLeuAspGlyTrpLeuIle 560
561	rpThr11eAlaValLeuAlaLeuThrCysAsnAlaLeuValThrSer

T; 0 U; 3 Other;

C; 918 G; 1352

BP; 1228 A; 1069

Sequence 4570

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The invention relates to a combination comprising CDNAs that are differentially expressed in response to steroid treatment. Also included are the following: a high throughput method for using a cDNA to detect differential expression of nucleic acids in a sample; and a high throughput method of screening molecules or compounds to identify a ligand that specifically binds a cDNA. The sample is from a subject with wilson disease and comparison of a strandard defines a stage of that disease. The high throughput method of screening molecules or compounds to identify a ligand that specifically binds a cDNA comprises: combining the combination with molecules or compounds under conditions to allow specific binding; and detecting specific binding between each cDNA and at specific binding; and detecting specific binding between each cDNA and to proteins. The combination is useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis or hepatitis. The present sequence represents a human cDNA which is differentially expressed in steroid-induced C3A liver cells. Note: The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for the data for this 
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ProProSerSerValProSerProAlaTyrProValThrGluSerCy8HisLeuSerSer
                                                                                                                                                                                                                        CCTCCCAGTTCCGTGCCATCACCAGCTTATCCAGTGACTGAGAGCTGCCATCTTTCCTCT
                                                                                              SerCysAspSerThrGlnAlaLeuValThrPheThrSerSerSerIleThrTyrAspLeu
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                                                                                                 This invention describes a novel human G-protein coupled glycoprotein hormone receptors are important in the endocrine system and HG38 may be involved in development and function of the skeletal muscle, spinal cord, placenta and to a lesser extent, the brain. The transgenic animal may be useful for studying tissue and temporal specific expression or activity of the HG38 receptor, as well as for studying the ability of a variety of compounds to act as modulators of HG38 receptor activity
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                                            ThrValPheArgSerProLeuTyrIleSerProIleLysLeuLeuIleGlyValIleAla
                                                             ACAGITITICAGATICCCCTCTGTACATITICCCCCCATIAAACTGTIAATIGGGGTCATCGCA
                                                                                                    AlaValAsnMetLeuThrGlyValSerSerAlaValLeuAlaGlyValAspAlaPheThr
                                                                                                                        GCAGTGAACATGCTCACGGGAGTCTCCAGTGCCGTGCTGGTGGTGTGGATGCGTTCACT
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The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY90643-Y90687), and to DNA encoding them (AAA30708-A30743) and AAA30775-A30779). The mutant proteins of the invention contain a contain a portion of the protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TM6). A non-endogenous anino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acid 8 N-terminal of an endogenous proline in TM6 to form a sequence X-CC (AA)15-Fro. The endogenous aproline in TM6 to form a sequence X-CC (AA)15-Fro. The endogenous anino acid is selected from Lys, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Pro may be endogenous, non-endogenous, or a mixture of endogenous and non-endogenous creaidues. The constitutively active GPCRs are useful for identifying antagonists and partial agonists for use as pharmaceutical contidating the roles of the receptors in normal and diseases and disorders associated with that receptors. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous ligands. Sequences AAA30709-AAA30775 and AAA30779 represent DNAs encoding the mutant human
                                                                                                                                   G protein-coupled receptor; GPCR; constitutively active;
intracellular loop 3; transmembrane domain 6; drug screening; agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
                                                                                                 DNA encoding human mutant G protein-coupled receptor HG38 (V765K)
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US-10-751-736-84 (1-907) x AAA30779 (1-2724)

Similarity:

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Query Match:

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AATTAAGTTTATCCTTCTGGTGGTAGTCCCACTTCCTGCATGTCTCAATCCCCTTCTCTA 2459	2400	qq
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Search completed: July 12, 2005, 08:18:07 Job time : 1325 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

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July 12, 2005, 07:56:07; Search time 2965 Seconds (without alignments) 1920.553 Million cell updates/sec
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Published Applications NA:*

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RESULT 1 US-10-251-385-263 US-10-251-385-263 Sequence 263, Application US/10251385 Publication No. US20030105292A1 GENERAL INFORMATION: APPLICANT: Behan, Dominic P. APPLICANT: Chalmers, Derek T. APPLICANT: Liaw, Chen W.	٠.	
TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G; TITLE OF INVENTION: Protein-Coupled; TITLE OF INVENTION: Receptors FILE REFERENCE: AREN-0040; CURRENT APPLICATION NUMBER: US/10/251,385; CURRENT FILING DATE: 2002-09-20; PRIOR APPLICATION NUMBER: US/9/170,496; PRIOR FILING DATE: 1998-10-13	onstitutively	Activated Human G

ALIGNMENTS

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                                                       TTTCCTGATTTAACTGGAAACTGCAAACCTGGAGAGTCTGACTTTAACTGGAGCACAGATC
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; SEQ ID NO 421 ; TENGTH: 2724 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-225-567A-421 Alignment Scores: 0	Qy 1 MetAspThrSerArgLeuGlyValLeuLeuSerLeuProValLeuLeuGlnLeuAlaThr 20 Db 1 ATGGACACCTCCCGGCTCGGTGTCCTGTCCTGTGCTGTG		81 LeuLeuProAsnProLeuProSerLeuArgPheLeuGluGluLeuArgLeuAlaGlyAsn) .ਜ ਵਾ ਜ ਵ	161 LeuthisSerLeuthrgHisLeuTrpLeutspasnhalaLeuThrGluIleProValGln 18 161 LeuthisSerLeuthrgHisLeuTrpLeutspasnhalaLeuThrGluIleProValGln 18 181 CIGCATTCCCTGAGGCTGGCTGGATGCGTTAACAGAAATCCCGTCCAG 54 181 AlaPheArgSerLeuSerAlaLeuGlnAlaMetThrLeutAlaLeuthibhis 20 181 AlaPheArgSerLeuthaLagagagagagagagagagagagagagagagagagaga	201 IleprohaptyralaphedlyasnLeuserSerLeuvalValLeuHisleuHishsnasnan
						RECEPTORS
Qy 641 GlyPheLeuSerIlePheAlaSerGluSerSerValPheLeuLeuThrLeuAlaAlaLeu 660 Db 1921 GGTTTTTTGCTTTTTGCTTCTGTTTTTCCTGCTTACTCTGGCCCTG 1980 Qy 661 GluArgGlyPheSerValLygTySerAlaLygPheGluThrLygAlaProPheSerSer 680 Db 1981 GAGCGTGGTTCTTGTGAAATTTCTGCAAATTTGAAACGAAAGCTCCATTTTCTAGC 2040 Qy 681 LeuLygValIleIleIlIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 721 SerThrWetGlyTyTMetValAlaLeuIleLeuLeuAsnSerLeuCysPheLeuWetMet 740 Db 2161 AGCACCATGGGCTACATGGTCGCTCTATCTTCCTTTGCTTCCTCATGATG 2220 Oy 741 ThrIleAlaTyThrIysLeuTytCYsAsnLeuAspLeuSlyAspLeuGluAsnIleTrp 760 Db 2221 ACCATGCCTACAGGAGACACCAGGAGACATTGCTGGAGATATTTGGACAGGAGACCTCGAGAATATTTGG	761 AspCysSerWetValLysHisIleAlaLeuLeuLeuPheThrAsnCysIleLeuAsnCys	801 IleLysPhelleLeuLeuValValProLeuProAlaCysLeuAsnBroLeuLeuTyr 801 IleLysPhelleLeuLeuValValProLeuProAlaCysLeuAsnBroLeuLeuTyr 2401 ATTAAGTTTATCCTTCTGGTGGTAGTCCCACTTCCTGCATGTCTCAATCCCTTCTTAAG 821 IleLeuPheAsnProHisPheLysGluAspLeuValSerLeuArgLysGluThrTyrVal	2461 ATCITCHARCCICACITIANGGAGGATICTGGTGAGCCIGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	881 ProproserSerValProSerProAlaTyrProValThrGluSerCysHisLeuSerSer 881 ProProSerSerValProSerProAlaTyrProValThrGluSerCysHisLeuSerSer 881 CCTCCCAGTTCCGTGCCATCACCAGCTTATCCAGTGACTGAC	SULT 2 SQUARY SQ

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PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-15
PRIOR PILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2002-01-08
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Sequence 157, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
APPLICAMT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; TILE REFERENCE: P 573 PC00
; CURENT APPLICATION NUMBER. US/10/482,029
; CURENT FILING DATE: 2603-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARF, Pareatin version 3.1
; SEQ ID NO 15-7
; LENGTH: 2.860
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	661 GluArgGlyPheSerValLysTyrSerAlaLysPheGluThrLysAlaProPheSerSer 680	701 LeudlyGlySerLysTyrGlyAlaSerProLeuCysLeuProLeuProPheGlyGluPro 720	741 ThrilealaTyrThriysLeuTyrCysAsnLeuAsplysGlyAspLeuGluAsnIleTrp 760	781 ProvalAlaPheLeuSerBheSerSerLeulleAsnLeuThrPheileSerProGluVal 800	### ### ##############################	861 SerCysAspSerThrGlnAlaLeuValThrPheThrSerSerIleThrTyrAspLeu 880	Qy 901 ValAlaPheValProCysLeu 907 	Sequence 48, Application US/10651237 Publication No. US20050048494A1 GENERAL INFORMATION: APPLICANT: Ortho-Clinical Diagnostics, Inc.
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Matches:
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Gaps:
APPLICANT: Wang, Yixin
TITLE OF INVENTION: Colorectal Cancer Prognostics
FILE REFERENCE: ADS-5003 US NP
CURRENT APPLICATION NUMBER: US/+Q/651,237
CURRENT FILING DATE: 2003-08-27
NUMBER OF SEQ ID NOS; 94
SOFTWARE, Patentin Vergion-3.1
SEQ ID NO 48
LENGTH: 2880
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DB:
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; ORGANISM: human
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QQ	829	GAACTAGGATTTCATAGCAACAATATCAGGTCGATACCTGAGAAAGCATTTGTAGGCAAC 888
ć	281	ProSerLeulleThrileHisPheTyrAspAsnProlleGlnPheValGlyArgSerAla 300
qa	889	CCTICTCTTATTACAATACAATTCCCATCCCAATTTGTTGGGAGATCTGCT 948
ò	301	PheGlnHisLeuProGluLeuArgThrLeuThrLeuAsnGlyAlaSerGlnIleThrGlu 320
qa	949	TTCAACATTTACCTGAACTAAGAACACTGACTCTGAATGGTGCCTCACAATAACTGAA 1008
ò	321	PheProAspLeuThrGlyThrAlaAsnLeuGluSerLeuThrLeuThrGlyAlaGlnIle 340
qq	1009	TITCTGAITTAACTGGAACTGCAAACCTGGAGAGTCTGACTTTAACTGGAGCACAGATC 1068
ò	341	SerSerLeuProGlnThrValCysAsnGlnLeuProAsnLeuGlnValLeuAspLeuSer 360
qq	1069	rcarcriccreaaccercrecaarcagriaccraarcrecaagrecracarcrercr 1128
ò	361	TyrksnLeuLeuGlukspLeuProSerPheSerValCysGlnLysLeuGlnLyslleAsp 380
qa	1129	TACAACCIATTAGAAGAITTACCCAGITTTICAGICIGCCAAAAGCITCAGAAAATTGAC 1188
ò	381	LeukrgHisAsnGluIleTyrGluIleLygValAspThrPheGlnGlnLeuLeuSerLeu 400
qq	1189	CTAAGACATAATGAAATCTACGAAATTAAAGTTGACACTTTCCAGCAGTTGCTTAGCCTC 1248
à	401	
qq	1249	cGATCGCTGAATTTGGCTTGGAACAAATTGCTATTATTCACCCCAATGCATTTTCCACT 1308
'n	421	LeuProSerLeulleLysLeuAspLeuSerSerAsnLeuLeuSerSerPheProlleThr 440
Dp	1309	TIGCCATCCCTAATAAAGCTGGACCTATCGTCCAACCTCCTGTCGTCTTTTCCTATAACT 1368
λŏ	441	GlyLeuHisGlyLeuThrHisLeuLysLeuThrGlyAsnHisAlaLeuGlnSerLeulle 460
qq	1369	GGGTTACATGGTTTAACTCACTTAAAATTAACAGGAAATCATGCCTTACAGAGCTTGATA 1428
ολ	461	SerSerGluAsnPheProGluLeuLysVallleGluMetProTyrAlaTyrGlnCysCys 480
qq	1429	TCATCTGAAAACTTTCCAGAACTCAAGGTTATAGAAATGCCTTATGCTTACCAGTGCTGT 1488
ćo	481	AlaPheGlyValCysGluAsnAlaTyrLysIleSerAsnGlnTrpAsnLysGlyAspAsn 500
qq	1489	GCATTTGGAGTGTGGGAATGCCTATAAGATTTCTAATCAATGGAATAAAGGTGACAAC 1548
č	501	SerSerMetAspAspLeuHisLysLysAspAlaGlyMetPheGlnAlaGlnAspGluArg 520
qa	1549	AGCAGTATGGACGACCTTCATAAGAAAGATGCTGGAATGTTTCAGGCTCAAGATGAACGT 1608
λō	521	AspleuGluAspPheleuLeuAspPheGluGluAspleuLysAlaleuHisSerValGln 540
qq	1609	gaccrigaagarriccrecrigacririgaegaagaccreaaagcccricarreaggeag 1668
ογ	541	CysSerProSerProGlyProPhelysProCysGluHisLeuLeuhspGlyTrpLeuIle 560
qq	1669	TGTTCACCTTCCCCAGGCCCCTTCAAACCCTGTGAACACCTGCTTGATGGCTGGC
ζó	561	ArgileGlyValTrpThrIleAlaValLeuAlaLeuThrCysAsnAlaLeuValThrSer 580
qq	1729	AGAATTGGAGTGTGGACCATAGCAGTTCTGGCTTAGTTAG
λ	581	ThrValPheArgSerProLeuTyr1leSerProlleLysLeuLeu1leGlyVallleAla 600
Dp	1789	carceca 1
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Alignment Scores:

Pred. No.:
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Percent Similarity:
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Best Local Similarity:
1
Query Match:
2
                                    TYPE: DNA
ORGANISM: human
                                                ; ORGANISM: hur
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Publication No. US20050048526A1

GENERAL INFORMATION:
APPLICANT: Ortho-Clinical Diagnostics, Inc;
TITLE OF INVENTION: Colorectal Cancer Prognostics
FILE REPERENCE: VDX-5702-619

CURRENT APPLICATION NUMBER: US/10/782,413

CURRENT PILING DATE: 2004-02-18

PRIOR APPLICATION NUMBER: 10/651,237
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PRIOR FILING DAVE: 2003-08-28
NUMBER OF SEQ ID NOS: 94
SOFTWARE: Patentin version 3.1
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US-10-295-027-443

Publication No. [20203022350A1

GENERAL INFORMATION: Assessment of GENERAL INFORMATION: APPLICANT: Affair Daniel

APPLICANT: Affair National APPLICANT: Ginsberg, Wendy W. APPLICANT: Ginsberg, Near C. APPLICANT: Hevezi, Peter A. APPLICANT: Mark, David H. APPLICANT: Warray, Richard APPLICANT: Warray, Richard APPLICANT: Wethode of Exceening for Modulators of Cancer TITLE OF INVENTION: Methode of Exceening for Modulators of Cancer TITLE OF INVENTION: Wethode of Diagnosis of Cancer TITLE OF INVENTION: WHORE: US/0/295,027

CURRENT FILING DATE: 2002-11-13

PRIOR PELING DATE: 2001-11-13

PRIOR APPLICATION NUMBER: US 60/332,464

PRIOR APPLICATION NUMBER: US 60/334,393

PRIOR PELING DATE: 2001-12-14

PRIOR PELING DATE: 200
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                                                                                                       HisGlyAlaTrpTrpGluAsnGlyValGlyCysHisValIleGlyPheLeuSerllePhe
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1627 ATAGCAGTTCTGGCACTTACTTGTAATGCTTTTGGTGACTTCAACAGTTTTCAGATCCCCT
                                                             GlyValSerSerAlaValLeuAlaGlyValAspAlaPheThrPheGlySerPheAlaArg
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Ouery Match: US-10-751-736-84 (1-907) QY 287 HisPheTyrad DD 787 CATTTCTATG QY 307 LeuArgThrId DD 907 ACTGCAAACC QY 327 ThrAlaAsnG DD 347 ValCysAsnG DD 347 ValCysAsnG OY 387 TyrGlulleL OY 387 TyrGlulleL OY 387 TyrGlulleL OY 447 HisLeuLysi DD 11207 CTGGACTATG OY 447 HisLeuLysi DD 11207 CTGGACTATG OY 447 HisLeuLysi OY 487 AsnalaTyrL OY 487 AsnalaTyrL OY 507 HisLysi OY 507 CTGACTATG OY 667 CTTGACTTG OY 67 TyrGlulleL OY 77 TyrGaACTAAAAT OY 788 ANDGCCTATG OY 67 TyrGlulleL OY 788 ANDGCCTATG OY 67 TyrGlulleL OY 67 TyrGlulleL OY 788 ANDGCCTATG OY 67 TyrGlulleL OY 68 TyrGlulleL OY 788 ANDGCCTATG OY 68 TyrGlulleL OY 78 TyrGlulleL	1567 CCCTT 567 I1eAJ 1627 ATAGG 587 LeuTy 1687 CTGTY 607 G1yVE 607 G1yVE 1147 GGAGT
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Llark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Reritera, S., Wango, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, White, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
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Direct Submitsation
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Homo sapiens GPR49 gene, VIRTUAL TRANSCRIPT, partial sequence,
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Copyright (c) 1993 - 2005 Compugen Ltd
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                                                                                       ASIDPHEProGluLeulysVallleGluMetProTyrAlaTyrGlnCysCysAlaPheGly
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784 PheLeuGerPheSerBerLeuilaAbnLeuThrPheileSerProGluValileLyBPhe 803 2350 TCTTGTGCTTCTCTCTTTTATAACTTTATATACTTTATCAGGGAAGTAATTAAGTTT 2409 2350 TCTTGTGCTTCTCTCTCTTTATAACTTTATACTTTATCAGGGAAGTAATTAAGTTT 2409 2410 ATCTTTGGTGGTAGCTCTCTCTGGAAGTAATTAAGTTT 2409 2410 ATCTTTGGTGGTAGCTCTCTCTGGAAGTAACTTTCTAGATTTTATAGGAAGAAGTAATTAAGTTT 2409 2410 ATCTTTGGTGGTAGCTCTCTCTGGAAGAAGAGAAGAGAA	2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: sequescope.cns.fr, Web: www.genoscope.cns.fr 1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ExcRY sites of the pCMVSFORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7021.f For more information about this cluster 7021.f For more information about this cluster 7021.f FATURES Source In 1060

Alignment Scores:

563 480 583 540 600 623 999

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1 (basea 1 to 590)

Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.

Circular rapid amplification of cDNA ends for high-throughput Genomics 84 (1), 205-210 (2004)
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                                                                                                                                                                                                                                                                                              ValTrpThr1leAlaValLeuAlaLeuThrCysAsnAlaLeuValThrSerThrValPhe
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            AspaspleutisLysLysAspAlaGlyMetPheGlnAlaGlnAspGluArgAspLeuGlu
                                                                                                       AspPheLeuLeuAspPheGluGluAspLeuLysAlaLeuHisSerValGlnCysSerPro
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3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
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1 (bases 1 to 800)

Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Caln, S., Leventhal, C., Thornton, M., Ramachandran, R., Mhittington, J., Lerner, L., Costanzo, D., McBligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Creation of genome-wide protein expression libraries using random activation of gene expression

122275151
800 bp mRNA linear EST 21-APR-2001
RST15934 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
BG196708
BG196708.1 GI:13718395
BST.
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Athersys, Inc.
3201 Carnegle Ave, Cleveland, OH 44115,
121 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
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EM Homo sapiens

EMIATORIA Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

EMIATORIA; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

ELI,W.B., Gruber; C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

IN Published (2001)

On Feb 13, 2001 this sequence version replaced gi:31068631.

Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage

I rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr web: www.genoscope.cns.fr

Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Econ V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
AL530798 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens AL530798 AL530798 AL530798 Homo sapiens AL530798
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                      RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seg primer:
Ml3r, Primer seguence: TTTCACACAGGAAACAGCTATGAC.
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I (bases I to 472)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le.N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               472 bp mRNA linear EST 09-JUN-1 zx68c09.r1 Soares total fetus ND2HF8 9w Homo sapiens cDNA clone IMAGE:796624 5' similar to WP:CS0H2.I CE05479 STEROID HORMONE RECEPTOR;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham.
Location/Qualifiers
1. .472
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CTGTCGTCTTTTCCTATAACTGGGTTACATGGTTTAACTCACTTAAAATTAACAGGAAAT
                                                   362 CATGCCTTACAGAGCTTGATATCATCTGAAAACTTTCCAGAACTCAAGGTTATAGAAATG
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                              HisAlaLeuGlnSerLeuIleSerSerGluAsnPheProGluLeuLysValIleGluMet
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4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
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bQ323949
IL5-CI0149-011100-224-a05 CI0149 Homo sapiens cDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                           Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Na and Eco RI sites of the modified pI713 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Patima Bonaldo. "
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/organism="Homo sapiens"
mol_type="mRNA"
db_xref="taxon:9608"
/db_xref="taxon:9606"
/clone="IMAGE:796624"
/dev_stage="8-9 weeks"
/lab_host="DH108"
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/tissue type="Stomach"
/cell type="Floating aggregates"
/cell type="Floating aggregates"
/cell tine="SNU-520"
/lab host="Topl0F"
/lab host="Topl0F"
/clone lib="S21SNU-520"
/lab host="Topl0F"
/clone lib="S21SNU-520"
/note="Organ: Stomach; Vector: pT218RP1; Site_1: EcoR1;
Site_2: Not1; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped incer mRNA was ligated with DNA-RNA linker including EcoR is site by treatment of T4 RNA ligase and the first strand I site by treatment of T4 RNA ligase and the first strand I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was adjusted to a DNA strand by Okayama-Berg method. The converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Toplof' by electroporation method. The cDNA libraries constructed by this method are full-length enriched CDNA library."
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.B., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
                                                                                                                                                                                                                                                                                                                      BM795259 671 bp mRNA linear EST 05-MAR-2002
K-EST0077025 S21SNU520 Homo sapiens cDNA clone S21SNU520-31-C01 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
LeuGlnAsnAsnGlnLeuArgHisValProThrGluAlaLeuGlnAsnLeuArgSerLeu
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Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
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Mismatches:
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Unpublished (2002)
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Matches:
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/clone="$21$NU520-31-C01"
/sex="F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
plate: 31 row: C column: 01
High quality sequence stop: 671.
Location/Qualifiers
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Percent Similarity:
Best Local Similarity:
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/mol_type="mRNA"
/db_trefe="mRNA"
/db_trefe="maxon:9606"
/dov_stage="matult"
/clone_lib="C10149"
/note="Organ: colon ins; Vector: pucl8; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
darived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
            1 (bases 1 to 556)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: +55-11-2704922
Email: asimpson001
Email: asimpson001
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5&t2=IL5-CI0149-01100-224-a05&t3=2000-11-01&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 GAGCCCGACGGCAGGATGTTGCTCAGGGTGGACTGCTCCGACCTCGGGGCTCTCGGAGCTG 267
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                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                               Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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High quality sequence stop: 48.
Location/Qualifiers
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AI367723 374 bp mRNA linear EST 15-FEB-1999 qv75h01.x1 NCI CGAP Utl Homo sapiens CDNA clone IMAGE:1987441 3' similar to TR:Q90674 Q90674 LUTEINIZING HORMONE RECEPTOR ;, mRNA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                      Single pass sequencing. Dases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified v cross match v0.990329.

Plate: SRG8004 row: J column: 17
Seq primer: GTAATACCACTACTATAGGG.
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Matches:
Conservative:
Mismatches:
Indels:
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov.
                                                                                                                                                                                                                           /organism="Sus scrofa"
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Smith, T. P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Fox, J., Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W.
A second set of porcine ESTs from a pooled-tissue normalized
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806271 WARC 3PIG Sus scrofa cDNA 5', mRNA sequence.
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Contact: Smith TPL
Contack: Smith TPL
WO Box 166, Clay Center, NE 68933-0166, USA
  Indels:
Gaps:
                                                                    US-10-751-736-84 (1-907) x BM795259 (1-671)
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212

261

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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 3883 Std Error: 0.00
Seq prime: -40UP from Gibco
High quality sequence stope: 329.
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Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"
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                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 358)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Homo sapiens
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                                                                                                                  Email: cgapbe-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Email: cgapbe-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D., Ph.D., CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1807 Std Brror: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 307.
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//note="Organ: uterus; Vector: pCWV-SPORT6; Site_1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"
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1 (bases 1 to 374)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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Mismatches:
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                                                             Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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2593 bp DNA linear GSS 16-DEC-2003
Pan troglodytes GPR49 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Reritera, S., Wango, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, White, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                     TrprrpGluAsnGlyValGlyCysHisValIleGlyPheLeuSerIlePheAlaSerGlu
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1. (bases 1 to 533)

1. (bases 1 to 533)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

The Gapbs-remail.nih.gov

Email: capabs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Gerg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: S60 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 405.
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Copyright (c) 1993 - 2005 Compugen Ltd.
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2105692 Total number of hits satisfying chosen parameters:

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Post-processing: Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ΙD	AAW93889	AAY90682	ABP81968	AB006467	ADC22783	ADE59150	ADE59153	ADG42628	ADH14256	ADN40013	ADN39531	ADN39628	AD029408	ADQ80369	ADR67868	AAY90687	ADC22797	ADH14270	ADF70480	ADG42629	AAW93890	ADB80464	ADN40012	ADN39166	AAY42169
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                            1 MDTSRLGVLLSLPVLLQLATGGSSPRSGVLLRGCPTHCHCEPDGRMLLRVDCSDLGLSEL
                                             MDTSRLGVLLSLPVILQLATGGSSPRSGVLLRGCPTHCHCEPDGRMLLRVDCSDLGLSEL
                                                                                PSNLSVFTSYLDLSMNN1SQLLPNPLPSLRFLEELRLAGNALTY1PKGAFTGLYSLKVLM
                                                                                                PSNLSVFTSYLDLSMNNISQLLPNPLPSLRFLEELRLAGNALTYIPKGAFTGLYSLKVLM
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AAY90682 standard; protein; 907 AA.

AAY90682

RESULT 2
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The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY90677 and AAAY90677 and AAAY90677 and AAAY90677 and AAAY9079). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (TC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, is substituted for an endogenous proline in IC3 at a position 16 amino acids N-terminal of an endogenous proline in IM6 to form a sequence X-C (AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or Ala, and is preferably Lys when the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Pro may be condepended in the constitutively active GPCRs are useful for identifying antagonists, agonists and partial agonists for use as pharmaceutical agonists for a particular GPCR are useful for reating diseases and discassed conditions. Antagonists for a particular GPCR are useful for reating diseases and discassed with that receptors in normal and diseases and discassed with the receptor. Because the novel mutant GPCR are constitutively active, they can be used directly for screening of compounds without the red for an best useful for the present sequence.
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                                                                        G protein-coupled receptor; GPCR; constitutively active;
intracellular loop 3; transmembrane domain 6; drug screening; agonist;
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100.0%; Score 907; I
Best Local Similarity 100.0%; Pred. No. 0;
Matches 907; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                       12-OCT-1999;
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                                                                                                                                                       Homo sapiens
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                                                                                                                   antagonist.
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New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
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                                                                                                                                                                              (LIFE-) LIFESPAN BIOSCIENCES INC.
                                                                                                                                                  19-DEC-2000; 2000US-0257144P.
                                                                                                                    19-DEC-2001; 2001WO-US050107
                                                           12,
                                                                                                                                                                                                            Roush CL,
                                                                                                                                                                                                                                                                                                                                    autoimmune diseases.
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                                                          WO200261087-A2.
                             Homo sapiens
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AFRSLSALQAMTLALNKIHHIPDYAFGNLSSLVVLHLHNNRIHSLGKKCFDGLHSLETLD
                                                          LINYNNLDEFPTAIRTLSNLKELGFHSNNIRSIPEKAFVGNPSLITIHFYDNPIQFVGRSA
                                                                                                                      FOHLPELRILINGASOITEFPDLTGTANLESLTLTGAQISSLPQTVCNQLPNLQVLDLS
                                                                                                                                                                              YNLLEDLPSFSVCQKLQKIDLRHNEIYEIKVDTFQQLLSLRSLNLAWNKIAIIHPNAFST
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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino caids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or articly for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs—The, antigenic peptides for GPCRs and antibodies are useful for detecting the presence or absence of corresponding GPCRs—The, antigenic peptides for GPCRs and antibodies are useful for detecting the presence or absence of corresponding GPCRs—The, antigenic peptides for GPCRs and antibodies are useful for detecting the presence or absence of corresponding GPCRs—The, antigenic peptides for GPCRs and antibodies are useful for detecting the regeneration-related disease, fimmunological-related call proliferative disease, or autoimmune diseases, eg. ALDS, Alzheimer's disease, corrections and acute inflammation, allergies, Crobn's disease, parkinson's disease, multiple sclerosis, pain, psoriasis, corrections or viral inflammation, allergies, Crobn's disease, pain, psoriasis, concertions or propersion, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis ABZ422859 encode GPCR proteins given in ABP81018, which are used in the present invention
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The invention relates to an isolated HGPRBMYS polypeptide. The polypeptides, polynucleotides and methods are useful for preventing, treating or ameliorating medical condition such as a neoplastic disorder e.g. bulkaemia and breast cancer; immune disorder e.g. AIDS and rheumatoid arthritis; neuronal disorder e.g. Alzheimer's disease and parkinson's disease; respiratory disorder e.g. bronchopulmonary disease and pancoast's syndrome; ovarian disorder e.g. ovarian carcinoma and meig's syndrome; colon disease; breast disease; thalamus related disorder; amygdala related disorder; corpus callosum related disorder; caudate nucleus related disorder; hippocampus related disorder by administering the GPCR polypeptide or its homologue. The present sequence represents the amino acid sequence of a G-protein coupled receptor used to show homology with the human G-protein coupled receptor, HGPCRBMY
                                                                                                                                                                                                                                                                                                                     New G-protein coupled receptor polypeptides, designated as HGPRBMYS, useful for preventing. treating or ameliorating a medical condition related to the coloh, preast, ovaries or immune system.
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                                                                 27-SEP-2000; 2000US-0235832P.
16-JAN-2001; 2001US-0261781P.
19-JUL-2001; 2001US-0306605P.
03-AUG-2001; 2001US-0310436P.
                          26-SEP-2001; 2001US-00965536.
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                  LNYNNLDEFPTAIRTLSNLKELGFHSNNIRSIPEKAFVGNPSLITIHFYDNPIQFVGRSA
                                         LNYNNLDEFPTALRTLSNLKELGFHSNNIRSIPERAFVGNPSLITIHFYDNPIQFVGRSA
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Query Match
100.0%; Score 907; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 907; Conservative 0; Mismatches
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Parkinson's disease; respiratory disorder; bronchopulmonary disease; pancoast's syndrome; ovarian disorder; ovarian carcinoma; colon disease; bened's syndrome; breast disease; thalamus related disorder; gene therapy; amygdala related disorder; corpus callosum related disorder; hippocampus related disorder.

US2003027323-A1

Homo sapiens

G-protein coupled receptor; GPCR; caudate nucleus related disorder; neoplastic disorder; leukaemia; breast cancer; immune disorder; AIDS; rheumatoid arthritis; neuronal disorder; Alzheimer's disease; receptor;

Human G-protein coupled receptor HG38.

(first entry)

13-AUG-2003

240 240 420

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120

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constitutively active version of an endogenous human gracellus.

Interintorly active version of an endogenous human gracellus.

Intracellular-3 (IC3) region, by substituting a specific amino acid in the TW6 region with a different amino acid, and testing for constitutive cativity. The method is useful for creating a constitutively active version of an endogenous human GPCR that comprises a transmembrane 6 region and an intracellular loop 3 region. The altered human GPCR polypeptides are useful for screening test compounds for identification of inverse agonists or partial agonists of GPCR polypeptides, which may have therapeutic uses. The altered GPCR may also be used in vivo or in vitro in biological research. A nucleic acid encoding the altered GPCR may be used to create a transgenic animal expressing the altered GPCR in may be used to create a transgenic animal expressing the altered GPCR human G protein-coupled receptor without the need for provision of a human G protein-coupled receptor without the need for provision of a creening of compounds that modulate the activity of a human G protein-coupled receptor without the need for provision of a screening of compounds against orphan receptors for which no ligand is currently known. This sequence represents a human GPCR polypeptide of the
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or human polymucleotides or a polymucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the
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spinal segmental nerve injury; chronic constriction injury;
spared nerve injury; SNI; Chung.
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(FARB ) BAYER AG.
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polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Ching), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                      cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical; NOVX-associated disorder; cancer; human; G protein coupled receptor 49.
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(RAST/) RASTELLI L.
(SHIM/) SHIMKETS R A.
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                                                                                             ERGESVKYSAKFETKAPFSSLKVIILLCALLALTWAAVPLLGGSKYGASPLCLPLPFGEP
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                                                                            ERGFSVKYSAKFETKAPFSSLKVIILLCALLALTMAAVPLLGGSKYGASPLCLPLPFGEP
                                                                                                                                           STWGYMVALILLINSLCFLMMTIAYTKLYCNLDKGDLENIWDCSMVKHIALLLFTNCILNC
                AVNMLTGVSSAVLAGVDAFTFGSFARHGAWWENGVGCHVIGFLSIFASESSVFLLTLAAL
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2001US-0334393P.

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2002US-0347349P.
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98US-00170496
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Matches 907; Conservative
                           LIAW C W.
BEHAN D P.
CHALMERS D T.
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Human; differential expression; cancer; angiogenic disorder; fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine.
AVNMLTGVSSAVLAGVDAFTFGSFARHGAWWENGVGCHVIGFLSIFASESSVFLLTLAAL
                                                                                                AVNMLTGVSSAVLAGVDAFTFGSFARHGAWWENGVGCHVIGFLSIFASESSVFLLTLAAL
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                                                                                                                                                                                                                                 The invention relates to nucleic acids and proteins (ADN38683-ADN40064) whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; antibodies which specifically bind a polypeptide of the invention; antibodies of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, antibodies are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease,
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                                                                                                                      Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300
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      Glynne R, Hevezi
I, Zlotnik A;
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      Gish KC, Gly
Wilson KE,
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                                                                                                                                                                                                   Claim 12; SEQ ID NO C383; 1385pp; English.
      Aziz N, Ginsburg WM,
Murray R, Watson SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                              2003-468649/44.
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                                                                                N-PSDB; ADN39796
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The invention relates to nucleic acids and proteins (ADN38683-ADN40064)

whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a determining the presence or absence of a pathological cell in a determining the presence or absence of a pathological cell in a continuous control or angiogenic or absence of a pathological cell in a determining the presence or absence of a pathological cell in those of the invention or by detecting a polypeptide of the invention; antibodies which specifically bind a nucleic acid of the invention; use of such antibodies for drug targeting; colypeptides and nucleic acids. The nucleic acids, polypeptides, and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, attentionated and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, retinal neovascularistation syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present
                                                                                                                                                                                   Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting
                                                 Hevezi PA;
                                            Gish KC, Glynne R, He Wilson KE, Zlotnik A;
                                                                                                                                                                                                                                                                                   Claim 12; SEQ ID NO A131; 1385pp; English.
                                                                                                                                                                                                              useful for diagnosing, prognosing or t
a nucleic acid in a biological sample.
                                            Ginsburg WM,
R, Watson SR,
EOS BIOTECHNOLOGY INC.
                                                                                                                 WPI; 2003-468649/44.
N-PSDB; ADN39530.
                                                                    Murray R,
                                              Aziz N,
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Sequence 907 AA;

Query Match

Query Match

Best Local Similarity 100.0%; Score 907; DB 7; Length 907;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 907; Conservative 0; Mismatches 0; Indels

ö 120 180 180 240 240 300 420 420 480 480 540 540 360 PSNLSVFTSYLDLSMNNISQLLPNPLPSLRFLEELRLAGNALTYIPKGAFTGLYSLKVLM 120 LNYNNLDEFPTAIRTLSNLKELGFHSNNIRSIPEKAFVGNPSLITIHFYDNPIQFVGRSA 300 9 9 AFRSLSALQAMTLALINKIHHIPDYAFGNLSSLVVLHIHNNRIHSLGKKCFDGLHSLETLD PSNLSVPTSYLDLSMINI SOLLPNPLPSLRFLEELRLAGNALTYI PKGAFTGLYSLKVLM LONNOLRHVPTEALONLRSLOSLRLDANHISYVPPSCFSGLHSLRHLWLDDNALTEIPVQ FQHLPELRTLTLNGASQITEFPDLTGTANLESLTLTGAQISSLPQTVCNQLPNLQVLDLS YNLLEDLPSFSVCQKLQKIDLRHNEIYEIKVDTPQQLLSLRSLNLAWNKIAIIHPNAFST LPSLIKLDLSSNLLSSFPITGLHGE/THLKLTGNHALQSLISSENFPELKVIEMPYAYQCC AFGVCENAYKI SNQWNKGDNSSMDDLHKKDAGMFQAQDERDLEDFLLDFEEDLKALHSVQ 481 AFGVCENAYKISNQWNKGDNSSMDDLHKKDAGMFQAQDERDLEDFLLDFEEDLKALHSVQ 1 MDTSRLGVLLSLPVLLQLATGGSSPRSGVLLRGCPTHCHCEPDGRMLLRVDCSDLGLSEL LONNOLRHVPTEALONLRSLOSLRLDANHISYVPPSCFSGLHSLRHLWLDDNALTEIPVQ AFRSLSALQAMTLALNKIHHIPDYAFGNLSSLVVLHLHNNRIHSLGKKCFDGLHSLETLD LNYNNLDEFPTAIRTLSNLKELGFHSNNIRSIPEKAFVGNPSLITIHFYDNPIQFVGRSA POHLPELRTLTLNGASQITEFPDLTGTANLESLTLTGAQISSLPQTVCNQLPNLQVLDLS YNLLEDLPSFSVCOKLOKI DLRHNEI YEI KVDTFQQLLSLRSLNLAWNKI AI IHPNAFST LPSL1KLDLSSNLLSSFP1TGLHGLTHLKLTGNHALQSL1SSENFPELKV1EMPYAYQCC Gaps ö Indels ö 19 121 181 181 241 241 301 361 421 481 61 121 301 361 421 a d 셤 셤 셤 a ઠે 셤 ò 원 Š 8 ò ઠે ð Š

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fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
inflammatory disease; autoimmune disease;
            CSPSPGPFKPCEHLLDGWLIRIGVWTIAVLALTCNALVTSTVFRSPLYISPIKLLIGVIA
                                                            AVNMLTGVSSAVLAGVDAFTFGSFARHGAWWENGVGCHVIGFLSIFASESSVFLLTLAAL
                                                                                                               ERGESVKYSAKFETKAPFESLKVIILLCALLALTMAAVPLLGGSKYGASPLCLPLPFGEP
                                                                                                                                                 STMGYMVALILLNSLCFLMMTIAYTKLYCNLDKGDLENIWDCSMVKHIALLLFTNCILNC
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                                               AVNMLTGVSSAVLAGVDAFTFGSFARHCAWWENGVGCHVIGFLSIFASESSVFLLTLAAL
                                                                                                 ERGFSVKYSAKFETKAPFSSLKVIILLCALLALTMAAVPLLGGSKYGASPLCLPLPFGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         retinal neovascularistation syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine.
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2001US-0340376P.
2002US-0347211P.
2002US-0347349P.
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2002US-0397775P.
2002US-0397845P.
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2001US-0334393P.
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13-FEB-2002;
20-FEB-2002;
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14-DEC-2001;
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12-APR-2002;
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G protein-coupled receptor; GPCR; drug screening; diagnosis;

transgenic mouse; neurological disorder; adrenal gland disorder;

colon disorder; intestinal disorder; ardiovascular disorder;

muscular disorder; blood disorder; immune disorder; bone disorder;

control disorder; blood disorder; immune disorder; cancer;

widney disorder; luter disorder; nutritive disorder; cancer;

widney disorder; terus disorder; prostate disorder; restis disorder;

control disorder; stomach disorder; proctate disorder; spleen disorder;

whymus disorder; thyroid disorder; antiparkinsonian; antimanic;

cytostatic; antiinflammatory; vasotropic; antidiarthoeic; antidiabetic;

wirucide; hepstotropic; antibacterial; antianaemic; antidiabetic;

dermatological; antiulcer; antibacterial; antianaemic; antiseborrhoeic;

munnosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
CSPSPGPFKRCEHLLDGWLIRIGVWTIAVLALTCNALVTSTVFRSPLYISPIKLLIGVIA
                                                                                                                                                                                                                                                                                    ERGFSVKYSAKFETKAPFSSLKVIILLCALLALTWAAVPLLGGSKYGASPLCLPLPFGEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                          PVAFLSFSSLINLTFISPEVIKFILLVVVPLPACLNPLLYILFNPHFKEDLVSLRKQTYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               841 WTRSKHPSLMSINSDUVEKQSCDSTQALVTFTSSSITYDLPPSSVPSPAYPVTESCHLSS
                                                                         CSPSPGPFKPCEHLLDGWLIRIGVWTIAVLALTCNALVTSTVFRSPLYISPIKLLIGVIA
                                                                                                                                                                  AVNMLTGVSSAVLAGVDAFTFGSFARHGAWWENGVGCHVIGFLSIFASESSVFLLTLAAL
                                                                                                                                                                                                             AVNWLTGVSSAVLAGVDAFTFGSFARHGAWWENGVGCHVIGFLSIFASESSVFLLTLAAL
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Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H;
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                                                                                                                                                                                                                                                                                                                                                                                             whose expression is upregnlated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention, antibodies which specifically bind a polypeptide of the invention, antibodies with specifically bind and methods of screening for modulators of activity or expression of the polypeptides and mucleic acids. The nucleic acids, polypeptides, antibodies and methods are useful for disgnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                                                       Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSNLSVFTSYLDLSMNNISQLLPNPLPSLRFLEELRLAGNALTYIPKGAFTGLYSLKVLM 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistation syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MDTSRLGVLLSLPVLLQLATGGSSPRSGVLLRGCPTHCHCEPDGRMLLRVDCSDLGLSEL
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                                                                                                    Glynne R, Hevezi
3, Zlotnik A;
                                                                                               Gish KC, Gly
Wilson KE,
                                                                                                                                                                                                                                                                                                                                                                               invention relates to nucleic acids and
                                                                                                                                                                                                                                                                                                                                    Claim 12; SEQ ID NO A228; 1385pp; English.
                                                                                                                                                                                                                                                                 useful for diagnosing, prognosing or tr
a nucleic acid in a biological sample.
                                                                                                    Ginsburg WM,
                                                      EOS BIOTECHNOLOGY INC
         09-SEP-2002; 2002US-0409450P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 907; Conservative
                                                                                               Aziz N, Gir
Murray R,
                                                                                                                                                                      WPI; 2003-468649/44
                                                                                                                                                                                              N-PSDB; ADN39627.
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                                                                                                    Afar D, #
Mack DH,
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Identifying a mammal that will respond therapeutically to a method of treating cancer comprises comparing the level of a biomarker in a mammal
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                                                                                                                                      421 LPSLIKLDLSSNLLSSFPITGLHGLTHLKLTGNHALQSLISSENFPELKVIEMPYAYQCC
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                             361 YNLLEDLPSFSVCQKLQKIDLRHNEIYEIKVDTFQQLLSLRSLNLAWNKIAIIHPNAFST
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YNLLEDLPSFSVCQKLQKIDLRHNEIYEIKVDTFQQLLSLRSLNLAWNKIAIIHPNAFST
                                                                                                               LPSLIKLDLSSNLLSSFPITGLHGLTHLKLTGNHALQSLISSENFPELKVIEMPYAYQCC
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                                                                                                                                                                                                                                                                                              The invention relates to human and mouse G protein-coupled receptors

(GPCRs) and nucleic acids encoding them. The invention also relates to
sequences at least 9% identical to the GPCR proteins and nucleic acids
of the invention, methods of treating, preventing or diagnosing diseases
of the invention, methods of treating, preventing or diagnosing diseases
compounds useful in the treatment of GPCR-related diseases; a transgenic
mouse comprising a GPCR gene of the invention; a mouse comprising
compounds useful in the treatment of GPCR-related diseases; a transgenic
mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
from the trasngenic mice; kits comprising several mice, each of which has
a mutation in a different GPCR gene of the invention; and kits comprising
probes which hybridise to GPCR polynucleotides of the invention. The
cinvention further discloses variants of the GPCR polypeptides and vectors
comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
diseases including neurological disorders (e.g., Alzheimer's disease,
disporders of the adrenal gland; disorders of the colon or intettine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (e.g., Crohn's disease, diarrachea, food poisoning or irritable bowel syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders; blood disorders (e.g., antoimmune disorders (e.g., autoimmune disorders or anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or arthritis, bone and joint disorders (e.g., osteoarthritis, rheumarcid arthritis, pout or osteoporosis); metabolic or nutritive disorders (e.g., obesity, enzyme deficiency-related diseases or vitamin deficiency-related diseases); and disorders of the kidney, liver, lung, bresst, ovary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR of the thyroid (e.g., cancers). The present sequence represents a GPCR of the of the printed specification; those sequences not shown were obtained in ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                         Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina
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; Pred. No. 0;
0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                   Claim 151; SEQ ID NO 510; 542pp; English.
                                                                                                                                                                                           pectoris, Parkinson's disease.
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Best Local Similarity 100.0%;
Matches 907; Conservative 0;
                          2004-390329/36
                                                       N-PSDB; ADO29923
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The invention relates to a method of identifying a mammal that will respond therapeutically to a method of treating cancer by administering an epidermal growth factor receptor (EGFR) modulator by comparing the level of a biomarker in a mammal before and after exposure to an EGFR modulator. The method comprises: (a) measuring, in the mammal, the level of at least one biomarker identified in the specification; (b) exposing the mammal to the EGFR modulator; and (c) measuring in the mammal the level of the biomarker, where a difference in the level in step (c) compared to step (a) indicates that the mammal will respond therapeutically to the method of treating cancer. The method and biomarkers are useful for identifying a mammal that will respond therapeutically to a method of treating cancer by administering an epidermal growth factor receptor (EGFR) modulator. This sequence corresponds to one of the biomarkers whose levels of expression is measured in the method of the invention.
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after exposure to an epidermal growth factor receptor (EFGR)
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Sequence 907 AA;

720

ERGFSVKYSAKFETKAPFSSLKVI ILLCALLALTWAAVPLLGGSKYGASPLCLPLPFGEP

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known as HG38. The HG38 protein and corresponding nucleic acid, may be used in the method of the invention for detecting colon or lung cancer. The first method involves performing an assay to determine the amount of Protein to standard, thus detecting expression of protein in sample.

HG38 in a sample of colon or lung tissue, and comparing the amount of protein to standard, thus detecting expression of protein in sample, where differential expression of protein in sample, where differential expression of protein in sample, where differential expression of protein in sample when compared with the standard is diagnostic of colon or lung cancer. The second method involves hybridizing a composition comprising the HG38 coding sequence, or its complement, and a labelling moiety, to nucleic acids of a sample of comparing complex, detecting hybridization complex formation to a standard, where the comparison reflects differential expression of the polynucleotide in the sample relative to the standard and is diagnostic of a colon or lung cancer. This first method enables earlier diagnosis before the patient is symptomatic. Anti-HG38 antibodies are useful for treating colon or lung cancer.
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ERGFSVKYSAKFETKAPFSSLKVIILLCALLALTMAAVPLLGGSKYGASPLCLPLPFGEP
                                  STMGYMVALILLINSLCFLMMTIAYTKLYCNLDKGDLENIWDCSMVKHIALLLFTNCILNC
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Length 907;
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Search completed: July 12, 2005, 07:51:17 Job time : 112 secs

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version 5.1.6 - 2005 Compugen Ltd. GenCore (c) 1993

- protein search, using sw model OM protein е Е

July 12, 2005, 07:38:42; Search time 29 Seconds (without alignments) 3009.262 Million cell updates/sec

US-10-751-736-84 907 1 MDTSRLGVLLSLPVLLQLAT......PAYPVTESCHLSSVAFVPCL 907 Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

283416 seqs, 96216763 residues

0 Word size : Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB A Post-processing: Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES		
Result No.	Score	Query	Length	DB	ID	Description	
1	907	100.0	907	2	JE0176	orphan G protein-c	
7	51	5.6	907	~	JG0193	G protein-coupled	
e	σ	1.0	195	~	AF2638	conserved hypothet	
4	σ	1.0	209	~	G97420	hypothetical prote	
S	6	1.0	580	~	S06057	gene ND1 intron 3	
9	6	1.0	869	~	A71400		
7	6	1.0	1978	~	S11251	hypothetical prote	
œ	80	6.0	162	N	F97440		
σ,	80	0.9	178	N	A87605		
10	80	6.0	179	7	S75434	/ hypothetical prote	
11	80	0.9	238	~	AD1368	amino acid ABC-tra	
12	80	6.0	267	N	AF3511	homospermidine syn	
13	80	6.0	293	~	B71686	RNA polymerase sig	
14	80	0.9	299	~	S61248	Ğ,	
15	8	6.0	299	7	A75591	hypothetical prote	
16	60		324	~	T20679		
17	80	6.0	329	7	H64143		
18	80	0.9	402	N	T15490	hypothetical prote	
19	8	0.9	431	N	H84392	O-acetyl homoserin	
20	60	6.0	467	N	D86583	ubiquinone oxidore	
21	80	0.9	467	~	E72040	probable sodium-tr	
22	89	6.0	478	N	875572	glucosyltransferas	
23	80		481	N	AD3020	homospermidine syn	
24	æ	6.0	481	~	E98264	homospermidine syn	
25	ω	•	538	Н	D64164	hypothetical prote	
26	80	0.9	671	~	D84648	probable disease r	
27	80	0.9	674	N	JC5104	transcription init	
28	80	0.9	678	7	C97114		
29	80	6.0	729	7	F86308	Similar to disease	

hypothetical prote NUD1 protein - yea	ന നറ	hypothetical prote hypothetical prote hypothetical prote	hypothetical prote NADH2 dehydrogenas hypothetical prote	hypothetical prote hypothetical prote hypothetical prote	
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ALIGNMENTS

the glycc Cross-references: UNIPROT:075473; GB:AF062006; NID:93366801; PIDN:AAC28019.1; PID:9336 Comment: This protein is a receptor for a novel class of glycoprotein ligands. C;Specjesf Homo sapiens (man)
C;Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
C;Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
C;Accession: JBD176
R;McDonald_r-rMang, R.; Bailey, W.; Xie, G.; Chen, F.; Caskey, C.T.; Liu, Q. Biochem. Biophys. Res. Commun. 247, 266-270, 1998
A;Title: Identification and cloning of an orphan G protein-coupled receptor of A;Reference number: JB0176; MUID:98308104; PMID:9642114
A;Accession: JB0176
A;Mclecule type: mRNA
A;Residues: 1-907 <MCD> orphan G protein-coupled receptor precursor - human Genetics:

A proposition: 12q22-23
F;1-1/Domain: signal sequence #status predicted <SIG>F;1-1/Domain: transmembrane #status predicted <TM1>F;594-616/Domain: transmembrane #status predicted <TM1>F;639-660/Domain: transmembrane #status predicted <TM3>F;631-701/Domain: transmembrane #status predicted <TM3>F;631-701/Domain: transmembrane #status predicted <TM4>F;725-744/Domain: transmembrane #status predicted <TM5>F;768-791/Domain: transmembrane #status predicted <TM5>F;803-824/Domain: transmembrane #status #status

Gaps ö DB 2; Length 907; 0; Indels Query Match 100.0%; Score 907; D Best Local Similarity 100.0%; Pred. No. 0; Matches 907; Conservative 0; Mismatches

1 MDTSRLGVLLSLPVLLQLATGGSSPRSGVLLRGCPTHCHCEPDGRMLLRVDCSDLGLSEL

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PSNLSVFTSYLDLSMANISQLLPNPLPSLRFLEELRLAGNALTYIPKGAFTGLYSLKVLM 120 9 1 MDTSRLGVLLSLPVLLQLATGGSSPRSGVLLRGCPTHCHCEPDGRMLLRVDCSDLGLSEL 61 셤 ઠે ò

120 LONNOLRHVPTEALQNIRSLQSLRLDANHISYVPPSCFSGLHSLRHLWLDDNALTEIPVQ 180 180 61 121 121 셤 g ઠે

300 240 240 181 AFRSLSALQAMTLALNKIHHIPDYAFGNLSSLVVLHLHNNRIHSLGKKCFDGLHSLETLD LINYNNLDEFPTAIRTLSNLKELGFHSINIRSIPEKAFVGNPSLITIHFYDNPIQFVGRSA 241 g ઠે 8

FQHLPELRTLTLNGASQITEFPDLTGTANLESLTLTGAQISSLPQTVCNQLPNLQVLDLS 360 301

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C;Accession: AF2638
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell., Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Bfer, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:QBUHZ5; GB:AE008688; PIDN:AAL41524.1; PID:g17738854; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
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G97420
hypothetical protein AGR_C_894 [imported] - Agrobacterium tumefaciens (strain C58, Cereo)
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A;Molecule type: DNA
A;Residues: 1-209 cNUR>
A;Cross.references: UNIPROT:Q8UHZ5; GB:AE007869; PIDN:AAK86320.1; PID:g15155438; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Green W1 intron 3 protein 2 - Podospora anserina mitochondrion C; Species: mitochondrion Podospora anserina S06057 B; Cummings, D.J.; Domenico, J.M.; Michel, F. R; Cummings, D.J.; Domenico, J.M.; Michel, F. A; Title: DNA sequence and organization of the mitochondrial ND1 gene from Podospora anse A; Reference number: S06056; MUID:89063443; PMID:3197134 A; Residues: 1-580 cCUM> A; Residues: 1-580 cCUM> A; Residues: 1-580 cCUM> A; Residues: 1-580 cCUM> A; Residues: mitochondrion A; Residues: mitochondrion
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.0%; Score 9; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches
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145 PRSGVLLRG 153
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                                                                                                                                                                                                                    A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-195 <KUR>
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JG0193
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G.Date: 23-0ul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C;Accession: JG0193
R;Hermey, G.; Methner, A.; Schaller, H.C.; Hermans-Borgmeyer, I.
Biochem. Biophys. Res. Commun. 254, 273-279, 1999
A;Title: JGentification of a novel seven-transmembrane receptor with homology to glycopr
A;Reference number: JG0193; MUID:99121227; PMID:9920770
A;Accession: JG0193
A;Accession: preliminary
A;Accession: preliminary
A;Residues: 1-907 <HRR>
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                                                                                                                                                        LPSLIKLDLSSNLLSSPPITGLHGLTHLKLTGNHALQSLISSENFPELKVIEMPYAYQCC
                                                                                                                                                                                                                                          AFGVCENAYKI SNQWNKGDNSSMDDLHKKDAGMFQAQDERDLEDFLLDFEEDLKALHSVQ
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1 Similarity 100.0%; Pred. No. 5.3e-42;
51; Conservative 0; Mismatches 0; Indels
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Matches 51; Conserv
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hypothetical protein AGR C 1201 [imported] - Agrobacterium tumefaciens (atrain C58, Cere C; Species: Agrobacterium tumefaciens
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C; Accession: F97440
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B., Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                            A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; WUID:21608551; PMID:11743194
A;Accession: P97440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIFROT:Q8U518; GB:AE007869; PIDN:AAK86479.1; PID:g15155627; GSPDB:G
C;Genetics:
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Dps family protein [imported] - Caulobacter crescentus
C;Space: So-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: A87605
R;Nierman, W.C; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-179 <SEN>
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0.9%; Score 8; DB 2
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches
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A,Map position: circular chromosome
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C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C;Accession: A71400
C;Accession: A71400
C;Accession: A71400
C;Accession: A71400
C;Accession: A71400
C;Accession: A71400
A;Authors: Mueller-Auer, B.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giell avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans C.; Chalwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal A;Reference number: A71400
A;Reference number: A71400
A;Reference number: A71400
A;Actuse; preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-669 <BEV>A;Residues: 1-669 <BEV>A;Cross-references: UNIPROT:023253; GB:297335; NID:g2244747; PID:e326857; PID:g2244748
C;Genetics:
A;Map position: 4COP9-4G3845
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AlReference number: S74322; MUID:97061201; PMID:8905231
AlAccession: S77257
Alstus: nucleic acid sequence not shown; translation not shown
Alfolocule type: DNA
Alfolocule type: DNA
Alfolocule type: 1-1978 (KAN>
Alfolocule sequence was submitted to the EMBL Data Library, June 1996
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hypothetical protein slll265 - Synechocystis sp. (strain PCC 6803)

A; Species: Synechocystis sp.

C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C; Accession: S77257

R; Kaneko, T; Sato, S; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996

A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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100.0%; Pred. No. 5.4;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.9
ive 0; Mismatches
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Best Local Similarity 100.
Matches 9; Conservative
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A;Genetic code: SGC3
C;Keywords: mitochondrion
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es 9; Conserv
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RESULT 15
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homospermidine synthase [imported] - Brucella melitensis (strain 16M)
C; Species Brucella melitensis
C; Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C; Accession: AF3511
C; Accession: AF3511
R; Delvecchio, V. G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, R; Delvecchio, V. G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, S; Decc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A; Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A; Reference number: AD3552; PMID:11756688
A; Reterence number: AD3552; PMID:11756688
A; Accession: AF7511
A; Status: preliminary
A; Meseldues: 1-267 *KUR>
A; Status: preliminary
A; Meseldues: 1-267 *KUR>
A; Genetimental source: strain 16M
C; Genetics:
A; Genetics:
A; Gene: BMEI10016
A; Map position: II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid ABC-transporter (permease) homolog lmo2348 [imported] - Listeria monocytogene C;Species: Listeria monocytogenes C;Species: D; John 101368 C;Accession: AD1368 C;Accession: AD1368 C;Accession: AD1368 C;Duchaud, E.; Durand, A.; Baquero, F.; Berche, P.; Bloecker J; Dones, L.M.; Karst, U. D; Jones, L.M.; Kanst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mahad, A;Authors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: AB1077; MUID:21537279; PMID:11679669 A;Accession: AD1368 A;Actus: preliminary A;Molecule type: DNA A;Residues: 1-218 cGLA> A;Accession: Lateria EGD-e C;Genetics: A;Genetics: A;Genetic
A,Cross-references: UNIPROT:P96006, EMBL:Y08257, NID:g170772, PID:e283869, PID:g170784d A,Experimental source: strain P2 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996 C,Genetics:
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A;Residues: 1-293 -AND>
A;Cross-references: UNIPROT:Q2ZDM4; GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA1476-
A;Experimental source: strain Madrid E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: rpoH; RP303
C;Superfamily: transcription initiation factor sigma katF; transcription initiation factor
F;55-287/Domain: transcription initiation factor sigma katF homology <KTF>
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C;Species: bovine herpesvirus 1
C;Species: bovine herpesvirus 1
C;Species: bovine herpesvirus 1
C;Species: bovine herpesvirus 1
C;Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 09-Jul-2004
C;Accession: S61248
R;VIcek, C.; Benes, V.; Lu, Z.; Kutish, G.F.; Paces, V.; Rock, D.; Letchworth, G.J.; Schi Submitted to the EMBL Data Library, January 1995
A;Description: Nucleotide sequence analysis of a 30-kb region of the bovine herpesvirus
A;Accession: S61248
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A;Residues 1.299 «VIC>
A;Cross-references: UNIRROT:065574; EMBL:Z48053; NID:9971311; PIDN:CAA88126.1; PID:99713.
C;Superfamily: varicella-zoster virus gene 53 protein
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C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change O9-Jul-2004
C;Accession: A75591
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; I, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mal S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                C;Accession: B'1686
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUD:99039499; PMID:9823893
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                                                                                                                                                                          RNA polymerase sigma-32 factor (rpoH) RP303 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
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ilarity 100.0%; Pred. No. 22;
Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches
191 VSSAVLAG 198
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A;Accession: A75591
A;Status: preliminary
A;Nolecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-299 <WHI>
A;Cross-references: UNIPROT:Q9RYGO; GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF1250
A;Experimental source: strain R1
C;Genetics:
A;Gene: DRA0358
A;Map position: 2
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PIR; JE0176; JE0176.
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GO; GO:0004930; F:G-protein coupled receptor activity; TAS.

GO; GO:0007186; P:G-protein coupled receptor activity; TAS.

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InterPro; IPR00313; LRR Lyp.

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R PFmn; PF00101; 7tm 1; 1.

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G-protein coupled receptor; Glycoprotein; Leucine-rich Signal; Transmembrane.
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:Cl30018C02 product:G protein-coupled receptor 49, f
                                                                                                                               insert sequence.
Mame-opta49;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
363 AA
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61 PSNLSVFTSYLDLSMANISQLLPNPLPSLRFLEELRLAGNALTYIPKGAFTGLYSLKVLM 120

MDTSRLGVLLSLPVLLQLATGGSSPRSGVLLRGCPTHCHCEPDGRMLLRVDCSDLGLSEL MDTSRLGVLLSLPVLLQLATGGSSPRSGVLLRGCPTHCHCEPDGRMLLRVDCSDLGLSEL

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori F., Indtani Y., Ishii Y., Itoh M., Kagawa I., Kaukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Nishi K., Nomura K., Ninagawa A., Shiraki T., Saqake Y., Tagami M.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
E. Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TO TISSUE-Head;

MEDLINE=C57BL/6J; TISSUE-Head;

MEDLINE=C57BL/6J; TISSUE-Head;

Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,

A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                         the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUB=Head; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                          SEQUENCE FROM N.A.
STRAIN=CS7BL/6G; TISSUB=Head;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Head;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/3505500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:1341817; Gpr49.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR. Nterm.
InterPro; IPR003591; LRR. Lyp.
Pfam; PF01462; LRRNT; 1.
Pfam; PF00560; LRR 1; 9.
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Head;
The FANTOM CONSOTTIUM,
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                                                                                                                                                                                                                                                                                  RIKEN PANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                 NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENTAL STAGE: Expressed from embryonic day 10.5 (E10.58) in the developping spinal cord and in the neuroepipithelia of the the developping spinal cord and in the neuroepipithelia of the the pattern changed rapidly.

SIMILARITY: Belongs to the G-protein coupled receptor 1 family. SIMILARITY: Contains 17 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last unotation update)
Leucine-rich repeat-containing G protein-coupled receptor 5 precursor (G protein-coupled receptor 49)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99121227; PubMed=9920770; DOI=10.1006/bbrc.1998.9882; Hermey G., Methner A., Schaller H.C., Hermens-Borgmeyer I.; I.i. Identification of a novel seven-transmembrane receptor with homology of glycoprotein receptors and its expression in the adult and
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBCELULAR LOCATION: Integral membrane protein.
-1- TISSUB SPECIFICITY: Expressed in the gonads, the adrenal gland, and in the brain. In the central nervous system expression is restricted to the olfactory bulb. In the adrenal gland detected only in the neural-crest derived chromomaffin cells of the medulat, but not in the cells of the adrenal cortex. In the gonads, the expression is high in Graafian follicle, but absent from primary and secondary follicles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. Biophys. Res. Commun. 254:273-279(1999).
-!- FUNCTION: Orphan receptor. It may be an important receptor for signals controlling growth and differenciation of specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                               203 DYAFGNLSSLVVLHLHNNRIHSLGKKCFDGLHSLETLDLNYNNLDEFPTAI 253
                                                                                                                                                                                                    DYAFGNISSLVVLHIHINNRIHSLGKKCFDGIHSLETLDINYNNLDEFPTAI 253
                                                                                                                                        ..
                                                                                                  Length 363;
                                                                                                5.6%; Score 51; DB 2; Length 363
100.0%; Pred. No. 1e-39;
ive 0; Mismatches 0; Indels
                                                          363 AA; 39879 MW; D5E2FC4449FCE2C0 CRC64;
                                                                                                                                                                                                                                                                                                                         907 AA
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InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR002131; Gphrmn_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Gpr49; Synonyme=Fex, Lgr5;
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InterPro; IPR003591; LRR_typ.
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SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_TYP; 6.
                                                                                                                                        51; Conservative
                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                         MOUSE
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InterPro;
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                                                          SEQUENCE
                                           Receptor.
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Matches
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Homo sapiens (Human)
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SEQUENCE
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Matches
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Pfam; PF00560; LRR; 16.
Pfam; PF01462; LRRNT; 1.
PRINTS; PR00137; GLYCHORMONER.
PRINTS; PR00137; GLYCHRPDDPSN.
PRINTS; PR00199; LEURICHRPT.
SMART; SM00169; LRR TYP; 8.
SMART; SM00131; LRRTY; 1.
PROSITE; PS00237; GPROTEIN RECEP FI 1; FALSE_NEG.
PROSITE; PS50262; G_PROTEIN RECEP FI 2; 1.
G_protein coupled receptor; Glycoprotein; Leucine-rich repeat; Repeat;
                                                                                                                                                                                                                                                                Leucine-rich repeat-containing G protein-
coupled receptor 5.
Extracellular (Potential),
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N-linked (GlCNAc. . . ) (Potential).
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 51; DB 1; Length 907; Pred. No. 2.1e-39;
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Extracellular (Potential)
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Extracellular (Potential)
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Cytoplasmic (Potential).
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Cytoplasmic (Potential).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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TO T., Suzuki Y., Nishikawa T., Okayaki T., Sugiyama T., Irie R.,

A Wakamatsu A., Hayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

A Mammarco J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,

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A Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa B.,

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Pujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,

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Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,

Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
                                                                                                                                                                                                                                                                     . .; IEA.
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MEDIINE=20388592; PubMed=10935549; DOI=10.1210/me.14.8.1257;
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coupled receptors (LGR): identification of LGR6 and LGR7 and the
signaling mechanism for LGR7.";
Moi. Endocrinol. 14:1257-1271(2000).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Malek M., Globanu D.C., Rothschild M.F.;
Submitted (DEC-2001) to the EMBL/Genbank/DDBJ databases.
Submitted (DEC-2001) to the EMBL/Genbank/DDBJ databases.
BMBL; AF455799; AAQ0721.1; --
GO; GO:0016601; C:innegral to membrane; IEA.
GO; GO:0016500; P:protein-hormone receptor activity; IEA.
GO; GO:0004912; P:receptor activity; IEA.
GO; GO:0001186; P:G-protein coupled receptor protein signalin.
InterPro; IPR00237; GPCR_Rhodpsn.
InterPro; IPR00231; GPRTMI receptor.
PRINTS; PR00373; GLYGHORMOMER.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Leucine-rich repeat-containing G protein-coupled receptor
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llarity 100.0%; Pred. No. 5.6e-17;
Conservative 0; Mismatches 0;
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Lett. 520:97-101(2002).
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Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
Nomiyama H., Satoh N., Takami S., Tersashima Y., Suzuki O.,
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Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
Nakasi K., Yada T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
T. "Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE; PS50262; G PROTEIN RECEP F1 2; FALSE NEG.
G-protein coupled receptor; Glycoprotein; Leucine-rich repeat; Repeat;
                                                                                                                                                                                                                                                                                                                                      Nat. Genet. 36:40-45(2004).
-!- FUNCTION: Orphan receptor.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
-!- SIMILARITY: Contains 11 leucine-rich (LRR) repeats.
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InterPro; IPR00111; Gphrmn_receptor.
InterPro; IPR001511; LRR.
InterPro; IPR003591; LRR_typ.
Pfam; PP00560; LRR; 12.
PRINTS; PR00373; GLYCHORNONER.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR00019; LEURICHRPT.
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LRR 4.
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LRR 6.
LRR 7.
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Genew; HGNC:19719; LGR6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Douel B., Dowd Baton D., Poster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Hamong A., Kim H.S., Klimowski L., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A. Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang Z., Goddard A., Wood W.I., Godowski P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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LRR 9.
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By similarity.
N-linked (GlcNAc. ..) (Potent N-linked (GlcNAc. ..) (Potent CSPTP -> MISPT (in Ref. 2).
W -> R (in Ref. 3).
W -> R (in Ref. 3).
W -> BS931445AA2D8B4 CRC64;
                                                                                                                                                                                                                                  2.0%; Score 18; DB 1; Length 828; 100.0%; Pred. No. 1.1e-07; ive 0; Mismatches 0; Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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100.0%; Pred. No. 1.2e-07;
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InterPro; IPR003591; LRR_typ.
Pfam; PR00560; LRR 1; 15.
PRINTS; PR00373; GIYCHORMONER.
PRINTS; PR000373; GPCRRHODOPSN.
PRINTS; PR00019; LEURICHRPT.
                                                                                                                                                                                                                                                                                                                     285 TIHFYDNPIQFVGRSAFQ 302
                                                                                                                                                                                                                                                                                                                                           285 TIHFYDNPIQFVGRSAFQ 302
                                                                                                                                                                                           89301 MW;
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SMART; SM00369; LRR_TYP; 14
                                                                                                                                                                                                               Query Match
Best Local Similarity luv...
Local 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gonadotropin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORFNames=UNQ6427;
Homo sapiens (Human)
                                                                                                                                                                                             828 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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CONFLICT
CONFLICT
SEQUENCE
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SEQUENCE
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Q6UY15;
                                               REPEAT
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SEQUENCE
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                                 Q9BYD7
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Q8BXS9
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A patchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleron M., Soarse M.B., Bonaldon M.F., Carahnoi P.L., Forenger C.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carahnoi P., Frange C.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carahnoi P., Prange C.,
Broknatein M.J., Widin T.B., Tooshiyuki S., Carahnoi P., Mullahy S.J.,
Broknate S., McKernan R.J., Maraka J.A., Gunzarene P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Nhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.R., Touchman J.W., Green E.D., Dickson M.C.,
Andriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Shenration and initial analysis of more than 15,000 full-length human
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GO; GO: 0016021; C: integral to membrane; IEA.
GO; GO: 0016021; C: integral to membrane; IEA.
GO; GO: 000186; P: G-protein-hormone receptor activity; IEA.
GO; GO: 000186; P: G-protein coupled receptor protein signalin. .; IEA.
InterPro; IPR00276; GPCR Rhodsen.
InterPro; IPR00131; Gphrm. receptor.
InterPro; IPR00131; Gphrm. receptor.
InterPro; IPR00131; IAR.
Pff R.
FROM : FROM : FROM : FR.
FROM : FROM : FROM : FR.
FROM : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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100.0%; Pred. No. 1.2e-07;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO47905; AAH47905.1; --
HSSP; Q9BZR6; 1P8T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                     923 AA
                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 TIHFYDNPIQFVGRSAFQ 258
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233 TIHFYDNPIQFVGRSAFQ 250
                                                                                                                                                                                                                                                                                    (TrEMBLrel. 24, C
(TrEMBLrel. 24, I
(TrEMBLrel. 26, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                  LGR6 protein (Fragment).
                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
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Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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0086VU0

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DD 101-01-00

DD 101-01-00

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RESULT 8

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OKAZE H., Hayashi A., Kozuma S., Saito T.;
SUBLI, AB049405; BAB39854.1; -.
HSSP; P25147; 1D0B.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016500; F:protein-hormone receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. ..; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR001311; Gphrmn_receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last amnotation update)
Mus musculus adult retina cDNA, RIKEN full-length enriched library,
clone:A930009A08 product:G PROTEIN-COUPLED RECEPTOR LGR4 homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 928;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=CS7BL/60; TISSUE=Retina;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/3505500;
RIKEN FANTOM CONSORTIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       928 AA; 100487 MW; 4C3364ADEA89C463 CRC64;
                                                           Last sequence update)
Last annotation update)
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100.0%; Pred. No. 1.2e-07;
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928 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Prec.
                                       Created)
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IRRO01611; LRR.
InterPro; IRR003591; LRR typ.
Fam, PRO0560; LRR 1; 15.
PRINTS; PR00373; GIZCHORNOBE.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR00019; LEURICHR.T.
SMART; SM00369; LRR_TYP; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285 TIHFYDNPIQFVGRSAFQ 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 TIHFYDNPIQFVGRSAFQ 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Meth. Enzymol. 303:19-44(1999).
                                       01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001).
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Matches 18; Conservative
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PRELIMINARY;
                                                                                                  VTS20631 (Fragment).
Name=VTS20631;
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STRAIN=C57BL/6J; TISSUE=Retina;

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01-OCT-2002
                                                                                            QBN537
                                                                                                             Q8N537
                                                             RESULT 10
                                                                            08N537
                                                                                                             MGD; MGI:1891468; Gpr48.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016500; F:protein-hormone receptor activity; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
                          the RIKEN Genome Exploration Research Group Phase I & II Team, "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                   STRAIN=C57BL/6J; TISSUB=Retina;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adachi J., Alzawa K., Akhautra T., Arakawa T., Bono H., Carninci P., Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayashida K., Hayashida K., Hayashida K., Hayashida K., Harozane T., Hayashida K., Imotani K., Ishii Y., Itoh M., Kogawa T., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saitoh R., Satioh H., Sakai C., Sakai K., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                              STRAIN-C57BL/64; TISSUE-Retina; MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibbata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa M., Ohara B., Watshiwagi K., Fujiwake S., Inoue K., Togawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKE integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 878;
8.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             878 AA; 96877 MW; 68E64B5EDEA11B37 CRC64;
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PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15; DB 2; Pred. No. 8.76 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro: IPR000276; GPCR Rhodpsn.
InterPro: IPR002131; Gphrmn_receptor.
InterPro: IPR001611; LRR.
InterPro: IPR001611; LRR.
InterPro: IPR001697; Znf_C2H2.
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100.0%; Pred
0; N
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PRINTS; PRO0237; GPCRHODOPSN.
PRINTS; PRO0019; LEURICHRPT.
SMART; SMO0169; LER TYP; 5.
PROSITE; PSS0262; G_PROTEIN RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 15; Conservative
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Pfam; PF00560; LRR 1; 1
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                             SEQUENCE FROM N.A.
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NON TER
SEQUENCE
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Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altauberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.P., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,

Boat C.B., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M., Soares M.B., Bonaldo M.F., Casrainci P., Prange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Morley K.C., Hale S., Garcia B.P., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia B. S., Sanchez N.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016500; F:protein-hormone receptor activity; IEA.
GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPCR Rhodgen.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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o. 0.0076;
0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUB-Brain;
Strauberg R.;
Strauberg R.;
Submitted (UN1-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC033039; AAH33039.1; --
HSSP; P25147; 1D0B.
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SWART; SMOODS9; LRR TYP; 5.
PROSITE; PSSO262; G_PROTEIN RECEP F1 2; 1.
PROSITE; PSO0028; ZINC FINGER C2HZ 1; UNKNOWN 1.
PROSITE; PSO0028; ZINC FINGER C2HZ 1; UNKNOWN 1.
                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
927 AA
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100.0%; Pred. No. 0.0
ive 0; Mismatches
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InterPro; IPR002131; Gphrmn_receptor.
                                                            Created)
PRT;
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InterPro; IPR000372; LRR Nterm.
InterPro; IPR003591; LRR_typ.
InterPro; IPR007087; Znf_C2H2.
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PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR00019; LEURICHRPT.
                                                        22,
22,
                                                                                                                     01-MAR-2004 (TrEMBLrel. 26,
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PRELIMINARY;
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Pfam; PF01462; LRRNT; 1
Pfam; PF00560; LRR 1; 1,
                                                            01-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                 Homo sapiens (Human)
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                                                                                                                                                    GPR48 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R InterPro; IPR001216; GPCR_Rhodpsn.
R InterPro; IPR001211; Gphrmn_receptor.
R InterPro; IPR001211; Gphrmn_receptor.
R InterPro; IPR001311; Gphrmn_receptor.
R InterPro; IPR001372; LRR Nterm.
R InterPro; IPR003391; LRR_typ.
R Pfam; PP001001; Trm_1; 1.
R Pfam; PP001001; Trm_1; 1.
R Pfam; PR00137; GLRRUT; 1.
R RRINTS; PR00137; GPCRHUDOPSN.
R PRINTS; PR00131; LEURICHRPT.
R SMART; SM0013; LERRIT; 1.
R SMART; SM0013; LERRIT; 1.
R SMART; SM00369; LERRIT; 1.
R PROSITE; PS00237; G PROTEIN RECEP_F1_2; 1.
R PROSITE; PS00227; G PROTEIN_RECEP_F1_2; 1.
R G-PROSITE; PS00227; G PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 282:757-764(2001).

-I- FUNCTION: Orphan receptor.

-I- SUBCELLULAR LOCATION: Integral membrane protein.

-I- SUBCELLULAR LOCATION: Expressed in multiple steroidogenic tissues:

-I ISSUE SPECIFICITY: Expressed in multiple steroidogenic tissues:

placente, ovary, testis and adrenal. Expressed also in spinal
cord, thyroid, stomach, trachea, heart, pancreas, kidney, prostate
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Leucine-rich repeat-containing G protein-
coupled receptor 4.
Extracellular (Potential).
1 (Potential).
Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                  Loh E.D., Broussard S.R., Kolakowski L.F. Jr.;
"Molecular characterization of a novel glycoprotein hormone G-protein-
                                                                                                                            Q9BXB1; Q9NYD1;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Leucine-rich repeat-containing G protein-coupled receptor 4 precursor (G protein-coupled receptor 48).
Name=GPR48; Synonyms=LGR4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and spleen.
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
-!- SIMILARITY: Contains 15 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Pancreas;
MEDLINE=21294803; PubMed=11401528; DOI=10.1006/bbrc.2001.4625;
                                                                                                              951 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF346711; AAK31153.1; -.
EMBL; AF346709; AAK31153.1; JOINED.
EMBL; AF346710; AAK31153.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF257182; AAF68989.1;
HSSP; Q9BZR6; 10ZN.
Genew; HGNC:13299; GPR48.
STANDARD;
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565
575
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                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          coupled receptor.";
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                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                LGR4 HUMAN
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28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Leucine-rich repeat-containing G protein-coupled receptor 4 precursor.
Name=Gpr48; Synonyms=Lgr4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                           -> S (in Ref. 1; AAF68989).
-> P (in Ref. 1; AAF68989).
-> S (in Ref. 1; AAF68989).
                                                                                                                                                                                                                                                                                                                                                                             Length 951;
                                                                                                                                                                                                                                                                                                                                                                   Score 13; DB 1; Lengtn July Pred. No. 0.0078;
                                   4 (Potential).
Extracellular (Potential).
5 (Potential).
6 (Potential).
6 (Potential).
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                        104460 MW; SEOC2DFCF22CA1BB CRC64;
2 (Potential).
Extracellular (Potential).
3 (Potential).
Cytoplasmic (Potential).
                                                                                                         Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                            (GlcNAc. .)
(GlcNAc. .)
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LERR 11.
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LERR 13.
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N-linked (GlCNAC.)
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                                                                                                (Potential)
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LRR
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Les 13; Conservative
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 341
366
387
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Q80T31
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Q80UB8
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      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch):
                                                                                                                                                                                                       SMART; SM00013; LRENT; 1.
SMART; SM00369; LRR TYP; 5.
PROSITIS; PS00237; G PROTEIN_RECEP_F1_1; FALSE_NEG.
PROSITIS; PS50262; G PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Leucine-rich repeat; Repeat;
                                                                                                                                                                                                                                                              Potential.
Leucine-rich repeat-containing G protein-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Potential).
(Potential).
(Potential).
(Potential).
(Potential).
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                                                                                                                                                                                                                                                                                                                                                      (Potential).
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N-linked (GlCN)
N-linked (GlCN)
N-linked (GlCN)
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LRR.
                                                                                                     InterPro; IPR00216; GPCR_Rhodpen.
InterPro; IPR002131; Gphrmn_receptor
InterPro; IPR001313; Gphrmn_receptor
InterPro; IPR003121; LRR_Nerm.
InterPro; IPR003591; LRR_LYp.
Pfam; PP001001; 7tm_1; 1.
Pfam; PP00560; LRR; 15.
Pfam; PR00560; LRR; 15.
PRINTS; PR00237; GPCRHODOPSN.
PRINTS; PR00219; LEURICHRPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                             104138 MW;
                                                                             EMBL; AF061443; AAC77910.1; -.
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SIGNAL 1 24
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628615; Gpr48
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1.4%; Score 13; DB 1; Length 951; 100.0%; Pred. No. 0.0078;

Query Match Best Local Similarity

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IX Vassilatis D.K., Hohmann J.G., Zeng H., Li F., Ranchalis J.E.,

AN Vassilatis D.K., Hohmann J.G., Zeng H., Li F., Ranchalis J.E.,

A Mortrud M.T., Brown A., Rodriguez S.S., Weller J.R., Wright A.C.,

A Bergmann J.E., Galtanaris G.A.,

The G protein-coupled receptor repertoires of human and mouse.";

The G protein-coupled receptor repertoires of human and mouse.";

The G protein-coupled receptor repertoires of human and mouse.";

REL, AYZ-5619; AAO85131.1; -.

REL, AYZ-5619; AAO85131.1; -.

ROG GO:0004972; F:receptor activity; IEA.

RICEPRO; IPR00161; LRR.

DR HIRTS; PR00019; LRR I; 4.

DR PRINTS; RN00169; LRR IYP; 2.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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"The G protein-coupled receptor repertoires of human and mouse."; Proc. Natl. Acad. Sci. U.S.A. 100:4903-4908(2003).

EMBL; AY255562; AA086074.1; --
GO; GO:0004872; F:receptor activity; IEA.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Leucine-rich repeat-containing G protein-coupled receptor 6
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                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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100.0%; Pred. No. 0.13;
ive 0; Mismatches
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(TrEMBLrel. 24, Last seqn
(TrEMBLrel. 25, Last anno
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208 NLSSLVVLHLHNN 220
                                                                      199 NLSSLVVLHLHNN 211
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Matches 11; Conservative
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Strauberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

MEDLINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;

Matauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

MIschul S.F., Zeeberg B., Bardener C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Bardener C.F., Bhat N.K.,

Mother R.E., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Datchenko L., Marusina K.R., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Schmutz J., Myers R.M., Butterfield Y.S.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

McTrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
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MGD, MGI:2441805; Lgr6.
MGD, MGI:2441805; Lgr6.
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0016500; F:protein-homone receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
InterPro; IPR002131; Gphrmn_receptor.
                                                                                                                                                                                                                   Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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0
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1.2%; Score 11; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 11; Conservative 0; Mismatches 0; Indels
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                                   162 · 162
162 AA; 17608 MW; C593128C551FBB24 CRC64;
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Last annotation update)
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STRAIN-Czech II; TISSUE-Mammary tumor;
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01-JUN-2002 (TrEMBLrel, 21, La
01-MAR-2004 (TrEMBLrel, 26, La
Lgré protein (Fragment).
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Sequence 278, App
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745, App
10391, A
19, Appl
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158, App
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4592, Ap
                                                                                                                               July 12, 2005, 07:48:53; Search time 25 Seconds (without alignments) 2708.268 Million cell updates/sec
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(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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                5.1.6
Compugen Ltd.
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US-10-101-464A-809
US-01-101-464A-809
US-09-482-273-158
US-09-543-601A-5153
US-09-482-273-260
US-09-361-443-4
US-09-361-443-2
US-09-361-443-2
US-09-361-443-2
US-09-361-443-2
US-09-361-443-2
US-09-361-423-2
US-09-949-01A-199
US-09-245-281-19
US-09-245-281-19
US-09-246-241-19
US-09-246-241-19
US-09-246-248-19
US-09-246-248-19
US-09-246-248-19
US-09-246-364-19
US-09-865-364-19
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-09-248-796A-23648
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US-09-513-999C-7456
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                GenCore version (c) 1993 - 2005
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seq length: 200000000
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Perfect
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4041, Ap
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11269, A
2694, Ap
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US-08-816-772-2

US-09-134-0105-011

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US-10-101-464A-563

US-09-489-039A-11223

US-09-540-11269

US-09-52-91A-23000

US-09-270-767-5694

US-09-270-767-5694

US-09-270-767-5691

US-09-270-767-5591

US-09-252-991A-21079

US-09-252-991A-21079

US-09-252-991A-21079

US-09-270-767-57047

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Best Local Similarity
Matches 907; Conserv
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		RESULT 2 US-09-170-496D-278 is Sequence 278, Application US/09170496D is Sequence 278, Application US/09170496D is Sequence 278, Application US/09170496D is GENERAL INFORMATION: is APPLICANT: Chalmers, Derek T. is TITLE OF INVENTION: Receptors is TITLE OF INVENTION: Receptors is TITLE OF INVENTION: AREN-0040 is CURRENT PAPLICATION NUMBER: US/09/170,496D is CURRENT PILING DATE: 1998-10-13 is SEQ ID NOS: 294	E 5 0 0 10 0 0 0

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APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Hieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2002-03-18
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-11
SHING RELING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOGTWARE: PEASEEG for Windows Version 4.0
SEQ ID NOS 989
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100.0%; Pred. No. 24;
ive 0; Mismatches
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TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: PZ030P1
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CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER FILING DATE: 1999-07-14
EARLIER FILING DATE: 1999-07-15
EARLIER FILING DATE: 1999-07-15
EARLIER FILING DATE: 1999-07-15
EARLIER RPLICATION NUMBER: 60/092,922
EARLIER PILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 558
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 8; Conservative
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; ORGANISM: Homo sapiens
US-09-482-273-258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ELSHOURBAGY, NABIL A
APPLICANT: LI XIAOTONG
TITLE OF INVERTION: NOWEL 7TM RECEPTOR (H2CAA71)
FILE REFERENCE: GH-70055-1
CURRENT APPLICATION NUMBER: US/09/153,593A
CURRENT FILING DATE: 1998-09-15
EARLIER APPLICATION NUMBER: 08/866,757
EARLIER FILING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 644
                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FEBACEGO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,757
FILING DATE: 30-MAY-1997
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.0%; Score 9; DB 2; Best Local Similarity 100.0%; Pred. No. 17; Matches 9; Conservative 0; Mismatches
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100.0%; Pred. No. 17;
ive 0; Mismatches
                                                                                                                                                                                                   APPLICALLON TO THE PILING DATE:
PILING DATE:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70055
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEPAX: 610-407-0701
TELEPAX: 610-407-0701
TELER: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 644 amino acids
LENGTH: 644 amino acids
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US-10-101-464A-809
; Sequence 809, Application US/10101464A
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Best Local Similarity 100.
Matches 9; Conservative
                         Diskette
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OMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   474 PYAYQCCAF 482
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ORGANISM: HOMO SAPIENS
US-09-153-593-2
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US-09-153-593-2
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GENERAL INFORMATION:

APPLICANT GATY Breeon et. al

APPLICANT GATY BREEON et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PREDMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

PILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US 60/117,747

PRIOR PILING DATE: 2000-01-27

PRIOR PILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SECOND 10334
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US-09-361-443-4

i Sequence 4, Application US/09361443

i Patent No. 6660275

i GENERAL INFORMATION:

APPLICANT: Ownen, Raymond P

TITLE OF INVENTION: CHLANYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: 19721-005 (AV-5)

CURRENT FILING DATE: 1999-07-26

PRIOR FLING DATE: 1999-07-26

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PATENTING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PATENTING DATE: 1998-07-27

SOFTWARE: PATENTING DATE: 1998-07-27

SOFTWARE: PATENTING DATE: 1998-07-27
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                                                                                                                                                                                                                                                                                                                                   Length 259;
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100.0%; Pred. No. 86;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                     Query Match 0.9%; Score 8; DB 4;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER PILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 260
LENGTH: 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 10334, Application US/09489039A; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Klebsiella pneumoniae
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; ORGANISM: Chlamydia pneumoniae
US-09-361-443-4
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Best Local Similarity 100.
Matches 8; Conservative
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US-09-482-273-260
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APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US 60/128,706
PRIOR PLILNG DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
LENGTH: 232
LENGTH: 232
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  GENERAL INFORMATION:
APPLICANT: Rosen al.
TITLE ROF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: PZ030P1
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: DCT/US99/15849
EARLIER FILING DATE: 1999-07-14
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,926
EARLIER APPLICATION NUMBER: 60/092,926
EARLIER APPLICATION NUMBER: 60/092,956
EARLIER APPLICATION NUMBER: 60/092,956
EARLIER PILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 167
LIENGTH: 207
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; Patent No. 6334631
; GENERAL INFORMATION:
APPLICANT: Rosen et al.
ITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: PZ030P1
CURRENT APPLICATION NUMBER: US/09/482,273
; CURRENT PILING DATE: 2000-01-13
; EARLIER APPLICATION NUMBER: PZT/US99/15849
; BARLIER FILING DATE: 1999-07-14
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100.0%; Pred. No. 53;
tive 0; Mismatches
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1. Sequence 5153, Application US/09543681A
9. Patent No. 6605709
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Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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COGANISM: Homo sapiens
US-09-482-273-167
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US-09-482-273-260
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DAT
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GENERAL INFORMATION:
APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Mitchell, Wayne
APPLICANT: Mitchell, Wayne
APPLICANT: To avis, Ronald
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REFERENCE: 2002-33-13
CURRENT APPLICATION NUMBER: US/09/438,185A
CURRENT APPLICATION NUMBER: US 60/108,279
PRIOR PILING DATE: 1998-11-12
PRIOR PILING DATE: 1998-11-12
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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; Patent No. 6812339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: CPn0743
US-09-438-185A-745
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LENGTH: 469
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Sequence 793, Application US/09198452A

Sequence 793, Application US/09198452A

GENERAL INFORMATION:

APPLICANT: GATIffais, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevering PILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 793

LENGTH: 469
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APPLICANT: Murdin, Andrew D
APPLICANT: Murdin, Andrew D
APPLICANT: Murdin, Andrew D
APPLICANT: Oomen, Raymond P
TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: 1971-005 (AV-5)
CURRENT APPLICATION NUMBER: US/09/361,443
CURRENT FILING DATE: 1999-07-26
PRIOR PLILNG DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO : 4
SEG ID 
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                                                        Length 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.9%; Score 8; DB 4; Length 467; Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                  0; Indels
                                                        Query Match 0.9%; Score 8; DB 4; Best Local Similarity 100.0%; Pred. No. 99; Matches 8; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09361443
Patent No. 6660275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-361-443-2
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US-09-198-452A-793
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US-09-438-185A-745
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US-09-361-443-2
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Compugen Ltd.
 GenCore version
Copyright (c) 1993 - 2005
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OM protein - protein search, using sw model

Run on:

July 12, 2005, 07:34:30; Search time 31 Seconds (without alignments) 2815.116 Million cell updates/sec

US-10-751-736-84

Title: Perfect score:

4702 1 MDTSRLGVLLSLFVLLQLAT......PAYPVTESCHLSSVAFVPCL 907 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 88 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
3: pir2:*
1: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	orphan G protein-c		follicle stimulati	follitropin recept	follitropin recept			follitropin recept				thyrotropin recept	thyrotropin recept	luteinizing hormon	lutropin-choriogon	thyrotropin recept	thyroid stimulatin	lutropin-choriogon	thyroid stimulatin	thyrotropin recept	lutropin-choriogon	thyroid stimulatin	hypothetical prote	G protein-coupled	insulin-like growt	insulin-like growt	synleurin - human	insulin-like growt	gene wheeler prote
SUMMARIES	CI	JE0176	JG0193	I45896	3N0898	JC2237	JC1493	A34548	JC4301	JC7361	QRHUFT	A42395	ORHURH	A40077	177463	A49744	148882	JC7390	A41344	JC5643	A35956	QRHUUT	JC7389	T20123	JC2033	JC1282	JC5239	JC7973	JC6128	T13852
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•	Query Match	100.0	85.6	13.8	13.8	13.7	13.7	13.5	13.4	13.3	13.2	12.8	12.6	12.6	12.5	12.5	12.4	12.3	12.2	12.1	12.0	11.9	11.4	10.8	10.4	9.1	9.0	8.9	9.8	9.8
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181 AFRSLSALQAMTLALNKIHHIPDYAFGNLSSLVVLHLHNNRIHSLGKKCFDGLHSLETLD 240

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LNYNNLDEFPTAIRTLSNLKELGFHSNNIRSIPEKAFVGNPSLITIHFYDNPIQFVGRSA 300 LINYNNLDEFPTAIRTLSNLKELGFHSNNIRSIPEKAFVGNPSLITIHFYDNPIQFVGRSA 300 301 FQHLPELRTLTLNGASQITEFPDLTGTANLESLTLTGAQISSLPQTVCNQLPNLQVLDLS 360

241 241

MEGF5 protein - ra	insulin-like growt	tlr protein - frui	glial cell membran	slit protein 2 pre	slit protein 1 pre	protein	hypothetical prote	G protein-coupled	leucine-rich-repea	Ras-binding protei	platelet membrane	hypothetical prote	chaoptin precursor	lysine carboxypept	neuronal leucine-r
T13953	A41915	T13887	A58532	B36665	A36665	T42218	T15864	S40241	AD1822	T42998	A60164	T30947	A29944	A34901	JC7763
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1523	605	1385	1091	1469	1480	1531	1066	1115	1119	559	260	572	1134	536	707
8.6	8.5	8.5	8.5	8.3	. 8	8.2	8.1	8.1	7.9	7.9	7.9	7.8	7.7	7.6	7.5
403	402	400.5	398	391.5	391.5	385.5	382.5	381.5	371	370	370	364.5	360.5	356.5	354.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Clacesion: UBOTT6

Archaella, T., Wang, A., Bailey, W.; Xie, G.; Chen, F.; Caskey, C.T.; Liu, Q.

Biochem. Biophys. Res. Commun. 247, 266-270, 1998

A;Title: IdeAtification and cloning of an orphan G protein-coupled receptor of the glyc.

A;Reference number: UE0176; MUID:98308104; PMID:9642114

A;Accession: UE0176

A;Molecule type: mRNA

A;Residues: 1-907 <MCD>
A;Cross-references: UNIPROT:075473; GB:AF062006; NID:93366801; PIDN:AAC28019:1; PID:933

C;Comment: This protein is a receptor for a novel class of glycoprotein ligands.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                Species: Homo sapiens (man)
Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
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F;1-21/Domain: signal sequence #status predicted <SIG>F;1-22/Domain: signal sequence #status predicted <TM1>F;524-658/Domain: transmembrane #status predicted <TM1>F;534-616/Domain: transmembrane #status predicted <TM2>F;639-660/Domain: transmembrane #status predicted <TM3>F;631-701/Domain: transmembrane #status predicted <TM4>F;725-744/Domain: transmembrane #status predicted <TM5>F;788-791/Domain: transmembrane #status predicted <TM5>F;803-824/Domain: transmembrane #status predicted <TM5>F;803-824/Domain: transmembrane #status predicted <TM7>F;803-824/Domain: transmembrane #status predicted <TM7
orphan G protein-coupled receptor precursor - human
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Matches 907; Conservative
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A;Gene: FSHR
C;Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat h
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                              LNYNNLDEFPTAIRTLSNLKELGFHSNNIRSIPEKAFVGNPSLITIHFYDNPIQFVGRSA
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G. Porcein-coupled receptor FEX - mouse
C; Species: Mus musculus (house mouse)
C; Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C; Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C; Accession: JG0193
R; Hermey, G.; Methner, A.; Schaller, H.C.; Hermans-Borgmeyer, I.
Biochem. Biophys. Res. Commun. 254, 273-279, 1999
A; Title: Jdentification of a novel seven-transmembrane receptor with homology to glycopx A; Reference number: JG0193
A; Reference number: JG0193
A; Accession: JG0193
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A; Residues: 1-907 <HER>
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                                                                                                           AFGVCENAYKI SNQWNKGDNSSMDDLHKKDAGMFQAQDERDLEDFLLDFEEDLKALHSVQ
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  YNLLEDLPSFSVCQKLQKIDLRHNEIYEIKVDTFQQLLSLRSLNLAWNKIAIIHPNAFST
                                           YNLLEDLPSFSVCQKLQKIDLRHNEIYEIKVDTFQQLLSLRSLNLAWNKIAIIHPNAFST
                                                                     LPSLIKLDLSSNLLSSFPITGLHGLTHLKLTGNHALQSLISSENFPELKVIEMPYAYQCC
                                                                                LPSLIKLDLSSNLLSSFPITGLHGLTHKLTGNHALQSLISSENFPELKVIEMPYAYQCC
                                                                                                                      AVNMLTGVSSAVLAGVDAFTFGSFARHGAWWENGVGCHVIGFLSIFASESSVFLLTLAAL
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85.3%; Pred. No. 2.8e-253;
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Matches 774; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 -----NWRR----QTSDLHPICNKSILRQEVDDMTQARGQRVSLAEDDEPSYAKGFD 327
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LSKFGCYEVQA-QTYRSETSSTAHN 664
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                                                                                                                                         10 LSLPVLLQLATGGSSPRSGVLLRGCPTH-CHCEPDGRMLLRVDCSDLGLSELPSNLSVFT
                                                                                                                                                                    SYLDLSMINISQLLPNPLPSLRF-LBELRLAGNALTYIPKGAFTGLYSL-KVLMLQNNQL
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                                                                                           Gaps
                                                                                           272;
F;71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology
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                                                                                           Matches 215; Conservative 140; Mismatches 300; Indels
                                             13.8%; Score 650; DB 2; 23.2%; Pred. No. 2.4e-34;
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Althernate names: Collide-stimulating macaque
NyAlternate names: Collide-stimulating macaque
C;Species: Macaca fasacicularis (crab-ating macaque)
C;Date: 10-Sep-1999 Heavurce_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: Wool988; S18452
B;Gromoll, J, Dankbar B.; Sharma, R.S.; Nieschlag, E.
B;Gromoll, J, Dankbar Cloning of the testicular follicle stimulating hormone receptor of the A;Reference number: JON898, MUID:94071854; PMID:7504463
A;Accession: NN0898, MUID:94071854; PMID:7504463
A;Accession: NN0898, MUID:94071854; PMID:7504463
A;Residues: 1-695 cRRO>
A;Residues: 1-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----DLPRNAI
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NyAlternate names: follicle stimulating hormone receptor
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: JC1493; I47080
C;Accession: JC1493; I47080
A;Reference Biochem. Biophys. Res. Commun. 190, 888-894, 1993
A;Title: Cloning of alternately spliced mRNA transcripts coding for variants of A;Reference number: JC1493; MUD:93176195; PMID:8439338
A;Accession: JC1493
A;Molecule type: mRNA
A;Residues: 1-695 <KHA>
                                                                                                                                      124 NOLRHVPTEALONLRSLOSIRLD-ANHISYVPPSCFSGLHSLRHLWLDDNALTEIPVQAF
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                                                                          --ELRFVLTKLRVIPKGAFSGFGDLEKIEISON
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Nilternate names: eFSHR
Cispecies: Equue caballus (domestic horse)
Cipate: 28-Ang-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
Cispecies: Equue caballus (domestic horse)
Cipate: 28-Ang-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
Richer Commun. 201, 201-207, 1994
Aircher Commun. 201, 201-207, 1994
Aircher Commun. 201, 201-207, 1994
Aircher Commun. 20237; MulD: 94256980; PMID: 8198575
Aircher Commun. 20237; MulD: 94256980; PMID: 8198575
Aircher Commun. 20237; MulD: 94256980; PMID: 8198575
Aircher Commun. 20237
Aircher Commun. 20237; MulD: 94256980; PMID: 918576
Aircher Commun. 20237
Fig. 2010 Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR3>
Fig. 2010 Domain: transmembrane #status predicted cTM3>
Fig. 2010 Domain: transmembrane #sta
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                               ANWRROISELHPICNKS--ILRQEVDYMTQTRGORSSLAEDNESSYSRGFDMTYAEFDYD
                                                                                                                   GISSYMKVSICLEMDIDSPLSQLYVMSLLVLNVLAFVVICGCYTHIYLTVRNPNIVSSSS
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  --DDLHKKDAGMFQAQDERD
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    -----WNKGDNSSM-
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A; Accession: A41729
A; Status: preliminary
A; Molecule type: DNA
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A;Cross-references: UNIPROT:P35379
A;Experimental source: testis
R;Yarney, T.A.; Sairam, M.R.; Ravindranath, N.; Payne, S.; Seidah, N.G.
R;Yarney, T.A.; Sairam, M.R.; 1993
A;Title: Molecular cloning and expression of the ovine testicular follicle stimulating ha;Reference number: 147080; MUID:93351750; PMID:8394255
A;Accession: 147080
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-695 xYAR,
A;Residues: 1-695 xYAR,
A;Residues: 1-695 xYAR,
C;Genetics:
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Best Local Similarity 23.0%; Pred. No. 8.1e-34;
Matches 213; Conservative 139; Mismatches 304; Indels 270; Gaps
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C; Species: Ratus norregicus (Norway rat)
C; Species: Ratus norregicus (Norway rat)
C; Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C; Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C; Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
B; Species of Part 1: Nikolics, K.; Segaloff, D.L.; Seeburg, P.H.
Mol. Endocrinol. 4, 525-530, 1990
A; Mille: The testicular receptor for follicle stimulating hormone: structure and functic A; Reference number: A34548 MUID:91125358; PMID:2126341
A; Molecule type: mRNA
A; Molecule t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-692 cHEC>
A; Cross-references: GB:S81198; NID:g245344; PIDN:AAB21415.1; PID:g245345
A; Note: sequence inconsistent with the nucleotide translation
A; Note: sequence inconsistent with the nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN:81117, NCBIN:81119, NCBIN:81121, NC
B; Davis, D.; Liu, X.; Segaloff, D.L.
Mol. Endocrinol. 9, 159-170, 1995
A; Title: Identification of the sites of N-linked glycosylation on the follicle-stimulati
A; Reference number: A57562; MUID:95295729; PMID:777696
A; Contents: annotation; glycosylation sites
C; Function:
A; Contents: annotation; glycosylation sites
C; Function:
A; Description: receptor that mediates the biochemical effects of follitropin
C; Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat homology cLRR1>
F; 16-56. Domain: signal sequence #status predicted cAHD>
F; 16-56. Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR2>
F; 16-145/ Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR3>
F; 16-145/ Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR3>
F; 16-186/ Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR5>
F; 16-186/ Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR3>
F; 172-193/ Domain: transmembrane #status predicted cTM2>
F; 180-218/ Domain: transmembrane #status predicted cTM2>
F; 180-2
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                                                                  TKIAKRMAMLIFTDFLCMAPISFFAISASLKVPLITVSKSKILLVLFYPINSCANPFLYA 627
                                                                                                                                                                                                                                                                                LFNPHFKEDLVSLRKOTYVWTRSKHPSLMSINSDDVEKOSCDSTQALVTFTSSSIT-YDL 880
                                                                                                                                                                                                                                                                                                                                                                                                              -LSKFGCYEVOAQTYRSETSFTAHNF 665
CSMVKHIALLLFTNCILNCPVAFLSFSSLINLTFISPEVIKFILLVVVPLPACLNPLLYI
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F;486-508/Domain: transmembrane #status predicted <TM4>
F;529-50/Domain: transmembrane #status predicted <TM5>
F;574-597/Domain: transmembrane #status predicted <TM5>
F;609-630/Domain: transmembrane #status predicted <TM6>
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functional expressionand chromo:

A;Title: The porcine follitropin receptor: cDNA cloning, A;Reference number: JC4301; MUID:96011644; PMID:7590277 A;Accession: JC4301

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repeat

of the G-protein coupled receptors. It has

A.Cross-references: GB:L31966
A.Experimental source: ovarian granulosa cells
C;Comment: This receptor belongs to the family ermatogenesis in male and oogenesis in female.

A; Residues: 1-694 <REM>

A; Molecule type:

VFTSYLDLSMANISQLLPNPLPSLRFLEERRIAGNALTY1PKGAFTGLYSL-KVLMLQNN 124
DVFQGASG 219
48
PVILDISRTKVHŠLPNHGLENIKKIRARSTYRIKKIPNLDKFVTIMEASLTYPSHČCAFA 279
VCENAYKISNQMNKGDNSSMDDLHKKDAGMFQAQDERDLEDF 525 :
LLDFEEDLKALHSVQCSPSPGPFKPCEHLLDGWLIRIGVWTJAVIALTCNALVTSTVFRS 585
- VTCSPKPDAFNPCEDIMGYNILRVLIWFISILAITGNTTVLVVLTTS 389
PLYISPIKLLIGVIAAVNMLTGVSSAVLAGVDAFTFGSFARHGAWWENGVGCHVIGFLSI 645
QYKLTVPRFLMCNLAFADLCIGIYLLLIASVDIHTKSQYHNYAIDMQTGAGCDAAGFFTV 449
FASESSVFLITLAALERGFSVKYSAKFETKAPFSSLKVIILLCALLALTMAAVPLLGGSK 705
FASELSVYTLTAITLERWHTITHAMQLECKVQLRHAASVMVLGWTFAFAAALFPIFGISS 509
9
YTHIYLTVRNPTIVSSSSDTKI 569
VKHIALLETNCILNCPVAFLSFSSLINLTPISPEVIKFILLTVVVPLPACLNPLLYILFN 824
9
Ĕ
ARKSHCSSAPRV 677
RESULT 8 JC4301 follitropin receptor - pig N;Alternate names: follicle-stimulating hormone receptor C;Species: Sus scrofa domestica (domestic pig) C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 21-Jan-2000 C;Accession: JC4301 R;Remy, J.J.; Labbib-Mansais, Y.; Yerle, M.; Bozon, V.; Couture, L.; Pajot, E.;
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8

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A Map position: 3 q2.2-q2.3

C. Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein of Superfamily: glycoprotein hormone receptor; transmembrane protein C. Superfamily: glycoprotein hormone binding #status predicted -HOB> (F. 1-365/Domain: follicle-stimulating hormone binding #status predicted -HOB> (F. 10-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR> (F. 10-94/Domain: transmembrane #status predicted cTML> (F. 10-94/Domain: transmembrane #status predicted cTML> (F. 10-94/Domain: transmembrane #status predicted cTML> (F. 10-95/Domain: transmembrane #status predicted cTMS> (F. 10-95/Domain: tra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --DNINIHTYERNSFMGL------SFESMILWLS------KNGIREIHNC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFNG-----TQLDEL-NLSDNDNLE---- 206
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llarity 22.4%; Pred. No. 3.6e-33;
Conservative 139; Mismatches 298; Indels 258;
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	Db 281 ERKKSEMHPICKSEY Qy 533LKALHSVQCSPSPEPERCHLLDGMLIRIGWHIAVLALTCNALVTSTVER 894 333 EFNYDYILCNEVHDVICFPRDAFNPCEDIMGDNTLRVIMLISILAITGNITVLVILIS 392 Qy 585 SPLYISPIKLLIGVIAAVNMLTGVSSAVLAGVDAFTFGSFAHGAMWENGVGGHVIGFLS 644 1	RESULT 10 ORHUFT (CALILITOPIN receptor precursor - human NyAlternate names: follicle stimulating hormone receptor (FSHR) NyContains: follitropin receptor precursor long splice form; follitropin receptor precursor long splice long splice long splice long splice long splice long splice long long long splice long long long long long long long long
Qy 673 ETKAPFSSLKVIILLCALLALTMAAVPLLGGSKYGASPLCLPLPFGEPSTMGYMVALILL 732 Db 477 QCKVQVRHAASIMLYGWIFAFTVALFPIFGISSYMKVSICLPMDIDSPLSQLYVVSLLVL 536 Qy 733 NSLCFLAMTIAYTKLYCNL-DKGDLENIWDCSMVKHIALLLFTNCILACPVAFLSFSSLI 791 Db 537 NVLAFVVIGGCYIHIYLTVRNPNIMSSSSDTKIAKRWAMLIFTDFLCMVPISFFAISASL 596 Qy 792 NLTFISPEVIKFILLVVVDLPACLNPLLYILFNPHPKEDLVSLRKQTYVWTRSKHPSLMS 851 Db 597 KVPLITVSKLKILLVVLFYPRINSCANPFLYAIFTKNFRRDVFIL	RESULT 9 JC7361 Folltropin receptor precursor - newt NAlternate names: follicle-stimulating hormone receptor C;Species: Cynops pyrrhogaster (newt) C;Accession: JC7361 R;Nakayama, Y.; Yamamoto, T.; Oba, Y.; Nagahama, Y.; Abe, S. Biochem. Biophys. Res Commun. 275, 121-128, 2000 A;Title: Molecular cloning, functional characterization, and gene exppression of a folling cochem. Biophys. Res Commun. 275, 121-128, 2000 A;Reference number: JC7361 A;Rocession: JC7361 A	P; 97. Poor Journal Continue Facture predicted (1702) F; 97. Poor Journal Facture predicted (1702) F; 97. Poor Journal Facture predicted (1702) F; 96. 190, 199, 267, 292 Binding site: carbohydrate (Asn) (covalent) #status predicted F; 46, 190, 199, 267, 292 Binding site: carbohydrate (Asn) (covalent) #status predicted Query Match 13.3

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      lutropin receptor - mouse
NiAlernate names: luteinizing hormone-choriogonadotropin receptor
CiSpecies: Mus musculus (house mouse)
CiSpecies: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
CiAccession: A42395
CiAccession: A42395
SiGdermann, T.; Birnbaumer, M.; Birnbaumer, L.
J. Biol. Chem. 267, 4479-4488, 1992
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                                                                    SVFTSYLDLSMNNISQLLPNPLPSLRFLEELRLAGNALTYIPKGAFTGLYSL-KVLMLQN
                                                                                                                                                    124 NOLRHVPTEALQNIRSIQSIRLD-ANHISYVPPSCFSGLHSLRHLWLDDNALTEIPVQAF
                                                                                                                                                                                                                                                                                                                    243 YNNLDEFPTAIRTLSNLKELGFHSNNIRSIPEKAFVGNPSLITIHFYDNPIQFVGRSAFQ
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Ayitile: Wolecular Coining of a truncated isoform of the human follicle stimulating horm follocular coining of a truncated isoform of the human follicle stimulating horm follocular coining of a truncated isoform of the human follicle stimulating horm follocular coining of a truncated isoform of the human follicle stimulating horm follocular coining of a truncated isoform of the human follicle stimulating horm follocular coining of a truncated isoform of the human follicle stimulating horm follocular coining of a truncated isoform of the human follicle stimulating horm follocular coining of a truncated isoform of the human follocular coining and sequencing of the human fell coining follocular coining and sequencing of the human fell coining follocular coining follocular coining and sequencing of the human fell coining follocular coining and sequencing of the human fell coining follocular coining and sequencing of the human fell coining follocular coining and sequencing of the human fell coining follocular coining and sequencing of the human fell coining follocular coining and sequencing of the human fell coining follocular coining and sequencing of the human fell coining and sequencing of the human fell coining follocular coining and sequencing of the human fell coining follocular coining and sequencing of the human fell c
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site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
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                     mone receptor expressed in L cells.

A;Reference number: A42395; MUD:92165799; PMID:1311310

A;Accession: A42395

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-700 cGUD>
A;Cross references: UNIPROT:P30730; GB:M81310; GB:M81316; NID:g198811; PIDN:AAA39432.1;
A;Note: sequence extracted from NCBI backbone (NCBIN:84664, NCBIP:84066)
C;Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat homology cLRR1>
C;Keywords: G protein-coupled receptor; transmembrane protein
P;54-77/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR3>
P;102-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR3>
P;128-152/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR3>
P;128-152/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR5>
P;180-201/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR5>
P;180-201/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR5>
P;180-202-226/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR6>
P;202-226/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR6>
coupling of the murine luteinizing hormone receptor to adenyl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.8%; Score 600; DB 2; Length 700;
31 Similarity 23.0%; Pred. No. 4.3e-31;
207; Conservative 143; Mismatches 320; Indels 230;
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thyrotropin receptor precursor - human (7.5HR)
C,Species: Homo sapiens (man)
C,Accession: A33789; A33786; A34052; A36120; S38280
R;Libert, F.; Lefort, A.; Gerard, C.; Parmentier, M.; Perret, J.; Ludgate, M.; Dumont, J.
B;Chem. B;Cphys. Res. Commun. 165, 1250-1255, 1989
A;Title: Cloning; sequencing and expression of the human thyrotropin (TSH) receptor: evl. A;Reference number: A33789; MUID:90121232; PMID:2610690
A;Accession: A33789
A;Astatuse nucleic acid sequence not shown; not compared with conceptual translation
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A;Accession: A36120
A;Accession: A36120
A;Status: not compared with conceptual translation
A;Status: not compared with conceptual translation
A;Residues: 1-129,'S',131,'AFS',135-195,'D',197,'F',199-256,'S',258-263,'A',265-305,'IET
A;Residues: 1-129,'S',131,'AFS',135-195,'D',197,'F',199-256,'S',258-263,'A',265-305,'IET
A;Residues: 1-129,'S', 131,'AFS',135-195,'D',197,'F',199-256,'S',258-263,'A',265-305,'IET
A;Residues: 1, puprez, L.; van Sande, J.; Cochaux, P.; Gervy, C.; Mockel, J.; Dumont, J.;
Nature 365, 649-651, 1993
A;Title: Somatic mutations in the thyrotropin receptor gene cause hyperfunctioning thyrc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Experimental source: thyroid adenomas
A;Note: mutations to Cys-619 or to Ile-623 in hyperfunctioning thyroid adenomas cause cc
C;Comment: See PIR:JC1319 for a splice form of thyrotropin receptor which lacks the sevo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A)Description: receptor that mediates the biochemical effects of thyrotropin C; Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat h C; Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; hormone rece
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the humar
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;Residues: 1-600, H', 602-764 <NAG>

;Residues: 1-600, H', 602-764 <NAG>

;Cross-references: GB:M31774; NID:9340003; PIDN:AAA36783.1; PID:9340004

;Misrahi, M.; Loosfelt, H.; Atger, M.; Sar, S.; Guiochon-Mantel, A.; Milgrom,

;Misrahi, M.; Loosfelt, H.; Atger, M.; Sar, S.; Guiochon-Mantel, A.; Milgrom,

;Misrahi, M.; Loosfelt, H.; Atger, M.; Sar, S.; Guiochon-Mantel, A.; Milgrom,

;Title: Clouhing, sequencing and expression of human TSH receptor.

;Reference number: A34052; MUID:90147730; PMID:2302212
                                                                                                                                                                                                   638
                                                                                                                                                                                                                                                                                                     882
                                                                                                                                                                                                                                                                                                                                                             519 LPMDVESTLSQVYILSILLLNAVAFVVICACYVRIYFAVQNPELTAPNKDTKIAKKMAIL 578
                                                                                                 831
                                                                                                                                                               VSL------RKQTYVWTRSKHPSLMSINSDDVBKQSCDSTQALVTFTSSSITYDLPP
                                                                                                 LFTNCILNCPVAFLSFSSLINLTFISPEVIKFILLVVVPLPACLNPLLYILFNPHFKEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: mRNA
A,Residues: 1-86,'L',88-764 <LIB>
A,Cross-references: UNIPROT:P16473
R,Nagayama, Y.; Kaufman, K.D.; Seto, P.; Rapoport, B.
Biochem. Biophys. Res Commun. 165, 1184-1190, 1989
A,Title: Molecular cloning, sequence and functional expression of
A,Reference number: A33786; MUID:90121223; PMID:2558651
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A;Map position: 14q31-14q31
A;Introns: 231/2
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A; Residues: 615-642 < PAR>
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A;Status: nucleic acid sequence not shown
A;Status: nucleic acid sequence not shown
A;Rebidues: nucleic acid sequence not shown
A;Rebidues: 1-764 <PRN-
A;Rebidues: 1-764 <PRN-
A;Cross-references: UNIPROT:P14763; GB:M29957; NID:g164098; PIDN:AAA30901.1; PID:g164099
R;Parmentier, M.; Libert, P.; Maenhaut, C.; Lefort, A.; Gerard, C.; Perret, J.; van Sand
Nucleic Acids Res. 17, 10493, 1989
A;Fitle: Nucleotide sequence of the dog thyrotropin receptor cDNA.
A;Reference number: S06933; MUID:90098886; PMID:2602159
A;Accession: S06933
A;Status: translation not shown
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Ajourdus: Tembratorion not biode.

Ajourdus: 1-764 < PA2.

Ajourdus: 1-764 | Particular | Particular | Particular |

Cj.Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein |

Fj.1-20/Domain: signal sequence #status predicted < ASIG.

Fj.1-74-10/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR1>

Fj.102-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR2>

Fj.102-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR3>

Fj.12-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR4>

Fj.12-156/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR4>

Fj.17-10.126/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR5>

Fj.17-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR5>

Fj.17-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR5>

Fj.17-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR5>

Fj.17-225/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR5>
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                                                                                                                                                                                                                                          692
                                       774
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                                                                                                                                                                                                                                                                                                              -----RKQTYVWTRSKHPSLMSINSDDVEKQSCDSTQALVTFTSSSITYDLPPS-SVP 886
                                                                                                                                                                                                                                                                                                                                                                              ---- KVTHDMRQGLHNM 735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOAMTLALNKIHHIPDYAFGNISSLVVIHIHNNRIHSLGKKCFDGLHSLETLDLNYNNLD 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unitariogin receptor precursor - dog
NyAlesmate names: thyroid-stimulating hormone receptor; TSH receptor
C; Species: Canis lupus familiaris (dog)
C; Date: 22-dan-1993 #text_change 09-Jul-2004
C; Date: 22-dan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C; Parcession: A40077; S06933
R; Parmentier, M.; Libert, F.; Maenhaut, C.; Lefort, A.; Gerard, C.; Perret, Science 246, 1620-1612, 1989
A; Title: Molecular cloning of the thyrotropin receptor.
A; Reference number: A40077; MUID:90084524; PMID:2556796
                                                                                                                                                                                                                 : | |::| : |::| | : | : |: | DFICMARISFYALSAILINKPLITVSKILLVLFYPLNSCANPFLYAIFTKAFQRDVFIL
                                                                          NCILNCPVAFLSFSSLINLTFISPEVIKFILLVVVPLPACLNPLLYILFNPHFKEDLVSL
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                                       -- DKGDLENIWDCSMVKHIALLLFT
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EDVYELIENSHLT 748
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F;1-21/Domain: signal sequence #status predicted <SIG>
F;2-764/Product: thyrotropin receptor #status predicted <WAT>
F;2-764/Product: thyrotropin receptor #status predicted <WAT>
F;3-76/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRI>
F;77-101/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRI>
F;102-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRI>
F;127-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>
F;127-156/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>
F;127-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>
F;201-226/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>
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F;451-473/Domain: transmembrane #status predicted <TM3>
F;486-517/Domain: transmembrane #status predicted <TM3>
F;580-60/Domain: transmembrane #status predicted <TM4>
F;580-60/Domain: transmembrane #status predicted <TM5>
F;680-602/Domain: transmembrane #status predicted <TM5>
F;680-602/Domain: transmembrane #status predicted <TM5>
F;661-682/Domain: transmembrane #status predicted <TM5>
F;61-682/Domain: transmembrane #status predicted <TM5>
F;77,99,113,177,198,302/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 NOLRHVPTEALONLRSLOSLRLDANHISYVPPSCFSGLHSLRHLWLDDNALTEIPVOAFR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 SLSALQAMTLALNKIHHIPDYAFGNLSSLVVLHLHNNRIHSLGKKCFDGLHSLETLDLNY 243
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F;153-177/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrr> Query Match Best Local Similarity 22.6%; Pred. No. 2.4e-30; Matches 205; Conservative 143; Mismatches 309; Indels 251; Gaps 25;</lrr>	OY 6 LGVLLSLPVILQLATGGSSPRSGVILRGCPTHCHCEPDGRMLLRVDCSDLGLSELPSNLS 65	QY 66 VFTSYLDLSMINISQLLPNPLPSLRFLEELRLAGNALTYIPKGAFTGLYS-LKVLMLQNN 124	QY 125 QLRHVPTEALQNLRSLQSLRL-DANHISYVPPSCFSGLHSLRHLWLDDNALTEIPVQAFR 183	CY 184 SLSALQAMTLALNKIHHIPDYAFGNLSSLVVLHLHNNRIHSLGKKCFDGLHSLETLDLMY 243 Db 135CNTGIRTLPDVTK 147	QY 244 NNLDBFPTAIRTLSNLKELGFHSNNIRSIPEKAFVG-NPSLITIHFYDNPIQFVGRSAFQ 302	QY 303 HLPELRTLTLNGASQITEFPDLTGTANLESLTLTGAQISSLPQTVCNQLPNLQVLDLSYN 362 	Qy 363 LLEDLPSFSVCQKLQKIDLRHNEIYEIKVDTFQQLLSLRSLNLAWNKIAIIHPNAFST 420	Qy 421 LPSLIKLDLSSRNLLSSFPITGLHGLTHLKLTGNHALQSLISSENFPELKVIEMPYAYQCC 480	Qy 481 AFGVCENAYK-ISNQWNKGDNSSMDDLHKKDAGMFQAQDERDLEDFLL 527	GY 528 DFEEDLKALHSVQCSPSPGPFKDCEHLLDGWLIRIGVWTIAVLALTCNALVTSTVFRSPL 587 ::: : ::: :	CY S88 YISPIKLLIGVIAAVNMLTGVSSAVLAGVDAFTFGSFARHGAWWENGVGCHVIGFLSIFA 647 ::: ::	QY 648 SESSVFLLTLAALBRGFSVKYSAKFETKAPFSSLKVIILLCALLALTWAAVPLLGGSKYG 707	514 514 767 574 827 634 634 691
Db 88 TLQRLESHSFYNLSKØTHIEIRNTRSLTSID 118	Qy 308 RTLTLAGASQITEPPDLTGTANLESLTLTGAQISSLPQTVCNQLPNLQVLDLSYNL 363	Qy 364 LEDLPSFSVCQKLQKIDLRHNEIYEIKVDTFQQLLSLRSLNLAMNK-IAIIHPNAFSTL- 421 Db 187NGFTSIQGHAFNG-TKLDAVYLNKNKYLSAIDKDAFGGVY 225	Qy 422PSLIKLDLSSNLLSSFPITGLAGLTHLKLTGNHALQSLISSENFPELKVIEMPYAYQC 479	Qy 480 CAFGVCENAYKISNQWNKGDNSSMDDLHKKDAGMF 514	Qy 515 QAQDEREDLEDFLLDFBEDLKALHSVQCSFSPG 546	Qy 547 PFKPCEHLLDGWLIRIGVWTIAVLALTCNALVTSTVFRSPLYISPIKLLIGVIAAVNWLT 606	Qy 607 GVSSAVLAGVDAFTFGSFARHGAWWENGVGGHVIGFLSIFASESSVFLLTLAALERGFSV 666	Qy 667 KYSAKFETKAPFSSLKVIILLCALLALTWAAVPLLGGSKYGASPLCLPLPFGEPST 722 ::::	Qy 723 MGYMVALILLANSLCFLAMTIAYTKLYCNLDKGDLENIWDCSMVKHIALLLFTNCI 777 : :::: : ::: : :: Db 580 LAXIILVLLLNIVAPIIVCSCYVKIYITVRNPQYNPGDKDTKIAKRANVLFTDFM 635	Qy 778 LNCPVAFLSFSSLINLTFISPEVIKPILLVVPLPACLAPLLYILFNPHFKEDLVSL 834 1: 1: 1: 1: 1: 1: 1: 1	Qy 835RKQTYVWTRSKHPSLMSINSDDVEKQSCDSTQALVTFTSSSITYDLPPSSVPSPAY 890 696 FGICKRQAQAY-RGQRVSPKNSAGIQIQKVTRDMRQSLPNMQDEY 739	Oy 891 PVTESCHLS 899 : Db 740 ELLENSHLT 748	SULT 14 7463 7463 Freinizin Species: Daccessio Accessio Accessio Accessio Accessio Accessio Cell. Title: B Title: B Title: B Tritle: B T

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                                                                                                                                                                               VFTSYLDLSMNNISQLLPNPLPSLRFLEELRLAGNALTYIPKGAFTGLYS-LKVLMLQNN 124
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             LGVLLSLPVLLQLATGGSSPRSGVLLRGCPTHCHCEPDGRMLLRVDCSDLGLSELPSNLS
                                                                                       14 LAVLLIKPSQLQ----SRELSG---SRCPEPCDCAPDG--ALRCPGPRAGLARL----
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Appearance 1-100 (ALD)

Appearance 
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                                                                                                                                                                                                                                                                                                               the
lutropin-choriogonadotropin receptor precursor - rat

NyAlternate names: luteinizing hormone-choriogonadotropin receptor
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-May-1994 #sequence revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: A49744; A40545; Ā41343; A61453; A32460
R;Koo, Y.B.; Ji, I.; Slaughter, R.G.; Ji, T.H.
Endocrinology 128, 2297-2308, 1991
B,Aitle: Structure of the luteinizing hormone receptor gene and multiple exons of A;Reference number: A49744; MUID:91209270; PMID:2019252
A,Accession: A49744
A,Status: preliminary
A,Residues: preliminary
A,Residues: I-700 - KKOO-
MA,Residues: I-700 - KKOO-
MA,Residues: I-700 - KKOO-
MA,Residues: AFOO-
MA,Residues: AFOO
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Best Local Similarity
Matches 205; Conserv
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647

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BD075815 G protein
AR447625 Sequence
AR308745 Sequence
AR06144 Homo sapi
BD135244 Novel mam
AC07886 Homo sapi
AK075399 Homo sapi
AX016185 Sequence
AX016185 Sequence
AX016186 Sequence
AX106181 Mus muscu
BV208561 GPR49_209
AC129329 Mus muscu
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                                                                                                                                                                                                                                             AC126943 Mus muscu
AC126127 Rattus no
AC125943 Mus muscu
AC136417 Rattus no
AC16194 Sequence
AC1016194 Sequence
AC121055 Homo sapi
AC13055 Homo sapi
AC13055 Sequence
AC121055 Sequence
AC121055 Sequence
AC121055 Sequence
AC13055 AC16184 Sequence
AC13051 Novel goal
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AX542295 Sequence
AB049405 Homo sapi
CQ870634 Sequence
BCQ47905 Homo sapi
CQ840811 Sequence
AY358119 Homo sapi
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 7300 from Patent WO02068579.
CQ721366
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PE Corporation (NY) (US)
Location/Qualifiers
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Matches:
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                               BV208561
AC129329
AX658241
AF062006
AF062006
AF062006
AF061444
AF061444
AC078860
AK075399
AX01655
AX01655
AX01616
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AC126127
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TITLE
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-MODEL=frame+ p2n. model -DEV=x1h
-MODEL=frame+ p2n. model -DEV=x1h
-G-Cgn2_1/USFPC_spool/US10751736/runat_12072005_083640_22171/app_query.fasta_1.1095
-G-Cgn2_1/USFPC_spool/US10751736/runat_12072005_083640_22171/app_query.fasta_1.1095
-DECALLGRESOU - OFFWE SPOORE-GOLI.rge -MINNATCH=0.1 -LOOPCH=0 -LOOPEXT=0
-UNITS=bits -START=1 -ENDS=-1 -MATRIX=coligo -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -ENDS=-1 -MATRIX=0.0196
-NORM=ext -HEAPSIZEE=500 -MINLEN=0 -MAXLENE=2000000000
-USER=US10751736_@CGN 1 1_6632_@runat_12072005_083640_22171 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBICK=LNO -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRENES=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
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CQ766844 Sequence
AR308745 Sequence
AX549136 Sequence
                                                                                                              July 12, 2005, 07:53:17; Search time 9805 Seconds (without alignments) 4482.293 Million cell updates/sec
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                   - nucleic search, using frame_plus_p2n model
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                                                                                   OM protein
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No.
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Qy 701 LeuGlyGlyBerLysTyrGlyAlaSerProLeuCysLeuProLeuProPheGlyGluPro 720 Db 2101 CTGGGTGGCAGCAAGTATGGCGCTTCCTCTGCCTTTTGCCTTTTGGGAAGCCC 2160	Pred. No.: 0 Length: 2724 Score: 0 Matches: 907 Percent Similarity: 100.00\$ Mismatches: 0 Best Local Similarity: 100.00\$ Mismatches: 0
Qy 721 SerThrMetGlyTyrMetValAlaLeuIleLeuLeuAsnSerLeuCysPheLeuWetMet 740	100.00* Indels: 6 Gaps: (1-907) x CQ766844 (1-2724)
Qy 741 ThrIleAlaTyrThrLysLeuTyrCysAsnLeuAspLysGlyAspLeuGluAsnIleTrp 760 Db 2221 ACCATTGCCTACACCACTCTACTGCAATTTGGACAAGGGAACCTGGAGAATATTTGG 2280	Oy 1 MetAspThrSerArgLeuGlyValLeuLeuSerLeuProValLeuLeuGlnLeuAlaThr 20
Oy 761 AspCysSerMetValLysHisIlealaLeuLeuLeuPheThrAsnCysIleLeuAsnCys 780	Qy 21 GlydlySerSerProArgSerGlyValLeuLeuArgGlyCy8ProThrHisCy8HisCy8 40
Qy 781 ProValAlaPheLeuSerPheSerSerLeulleAsnLeuThrPheIleSerProGluVal 800	Qy 41 GlubroAspGlyArgMetLeuLeuArgValAspCysSerAspLeuGlyLeuSerGluLeu 60
Qy 801 IleLysPhelleLeuLeuValValValProLeuDroAlaCysLeuAsnBroLeuLeuTyr 820 Db 2401 ATTAAGTTTATCCTTCTGGTAGTCCCACTTCCTGCATCTCACTTCCCTTCTCTAC 2460	Qy 61 ProSerAenLeuSerValPheThrSerTyrLeuAepLeuSerMetAenAenIleSerGln 80
Oy 821 IleLeuPheAsnProHisPheLysGluAspLeuValSerLeuArgLysGlnThrTyrVal 840 Db 2461 ATCTTGTTCAATCCTCACTTAAGGAGATCTGGTGAGCTGAGAAAGCAAACCTACGTC 2520	Qy 81 LeuleuProAsnProAsnProSerLeuArgPheLeuGluGluLeuArgLeuAlaGlyAsn 100
Qy 841 TrpThrArgSerLysHisProSerLeuMetSerIleAsnSerAspAspValGluLysGln 860 Db 2521 TGGACAAGATCAAAACACCCAAGCTTGATGTCAATTAACTCTGATGATGTCGAAAAACAG 2580	Qy 101 AlaLeuThrTyrIleProLysGlyAlaPheThrGlyLeuTyrSerLeuLysValLeuMet 120
Qy 861 SerCysAspSerThrGlnAlaLeuValThrPheThrSerSerSerIleThrTyrAspLeu 880 Db 2581 TCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTATATGACCTG 2640	Qy 121 LeuGlnAsnAsnGlnLeuArgHisYalProThrGluAlaLeuGlnAsnLeuArgSerLeu 140
Qy 881 ProProSerSerValProSerProAladyrProValThrGluSerCysHisLeuSerSer 900	Qy 141 GlnSerLeuArgLeuAspalaAsnHisIleSerTyrValProProSerCysPheSerGly 160
Qy 901 ValAlaPheValProCysteu 907 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 161 LeuhisSerLeuhrgHisLeuTrpLeuAspAspAspAspAspAspAspAspAspAspAspAspAspA
RESULT 2 CQ766844 CQ766844 CQ766844 CQ766844 DBFINITION Sequence 3 from Patent W02004005457) CQ766844 CCBSSION	Oy 181 Db 541 Oy 201
REPERENCE 1 AUTHORS Colland, F., Barker, N., Clevers, J.C., Gomez, E., van de Wetering, M.L. and Suils, E.S. TITLE THE USE OF SPECIFIED TCF TARGET GENES TO IDENTIFY DRIGS. FOR THE	Oy 241 LeuasnTyrasnAsnLeuaspGluPheProThralalleargThrLeuSerAsnLeuLys 260
TREATMENT OF CANCER, IN PARTICULAR COLORECTAL CANCER, IN PARTICULAR COLORECTAL CANCER, IN PARTICULAR COLORECTAL CANCER, IN PACENT WO 2004005457-A 3 (15-JAN-2004); Kylix B.V. (NL)	Oy 261 GluLeuGlyPheHisSerAsnAsnIleArgSerIleProGluLysAlaPheValGlyAsn 280
COMMENT On Jun 7, 2004 this sequence Version replaced gi:44909056. FEATURES Location/Qualifiers Source 12724 /organism="Homo sapiens"	Oy 281 ProSerLeulleThrileHisPheTyrAspasnProlleGlnPheValGlyArgSerala 300
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Query Match: 100.00% Indelegates DB: 6 Gaps: US-10-751-736-84 (1-907) x AR308745 (1-2724) Qy 1 MetAspThrSerArgLeuGlyValLeuLeur Qy 1 ATGGACACCTCCCGGCTCGGTGTGCTCCTG Qy 21 GlyGlySerSerProArgSerGlyValLeur Qy 21 GlyGlySerSerProArgSerGlyValLeur Db 61 GGGGGCAGCTCTCCCCAGGTCTGGTGTGTTG	odlyargMetLeuLeuargVi 	roksnProLeuProSerLeuA 	.CATACATTCCCAAGGGAGCAT. SIASINGINLEUARGH.SVALP. 		rccridadaccridadactical rgserLeuserAlaLeuGlnA:	Asproximation of the control of the	HisSerLeuGlyLysLysCysP 	TyrasnasnLeuaspGluPheP: 	GlyPheHisSerAsnAsnIleA: 	LeulleThrileHisPheTyra 	HisLeuProGluLeuArgThrL	AspLeuThrGlyThrAlaAsnL	antitaaciggaacigcaaacc

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DD 2101 [THOROUGH	Alignment Scores: Pred. No.: Score: Score: Percent Similarity: 100.00\$ Mismatches: Mismatches: Alignment Scores: Degree 100.00\$ Mismatches: Mismatch
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Mammalia; Butheria; Primatee; Catarrhini; Hominidae; Homo.
1 (Bases 1 to 2880)
McDonald,T., Wang,R., Bailey,W., Xie,G., Chen,F., Caskey,C.T. and
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Identification and cloning of an orphan G protein-coupled confer the glycoprotein hormone receptor subfamily
Biochem. Biophys. Res. Commun. 247 (2), 266-270 (1998)
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McDonald,T., Wang,R., Bailey,W. and Liu,Q.
Direct Submission
Submitted (199.4PR-1998) Human Genetics, Merck Research |
Submitted (199.4PR-1998) Human Genetics, Merck Research |
Location/Qualifiers
1. 2880
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/db_xref="taxon:32644"
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		281 ProSerLeulleThrIleHisPheTyrAspAsnProlleGlnPheValGlyArgSerAla 300	961 TTTCCTGATTTAACTGCAAACCTGGAGGTCTGACTTTAACTGGAGGTC 1020 341 SerSerLeuProGlnThrValCysAsnGlnLeuProAsnLeuGlnValLeuAspLeuSer 360 341 SerSerLeuProGlnThrValCysAsnGlnLeuProAsnLeuGlnValLeuAspLeuSer 360 1021 TCATCTTCCTCAAACCGTCTGCAATCAGTTACCTAATCTCCAAGTGCTAGATCTTGTT 1080 361 TVAASnLeuLeuGluAspLeuProSerPheSerValCysGlnLysLeuGlnLyslleAsp 380	TACAACCTATTAGAAGATTTACCCAGTTTTTCAGTCTGCCAAAAGCTTCAGAAATTGAC LeuArgHisAsmGlulleTyrGlulleLysValAspThrPheGlnGlnLeuLeuSerLeu	CGATCGCTGAATTTGGCTTGGAACAAATTGCTATTATTCACCCCAATGCATTTTCCACT LeuProSerLeulleLysLeuAspLeuSerSerAsnLeuLeuSerSerPheProlleThr	1321 GGTTACATTAACTCACTTAAAATTAACAGGAATCCTTACAGAGGTTGATA 1380	1441 ĠCĂṛTṛTĠĠĠŢĠŢĠĠĠĀĀŢĠĊĊŢĀŢĀĠĀŢŢĊŢĀĀŢĊĀĀŢĠĠĀĀŢĀĀĀĢĠĀŢĠĀĠĀGĀ 1500 501 SerSerMetaspaspleuHisLysaspalaGlyWetPheglnAlaglnAspGluArg 520
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LaTyrPro	IIION Sequence 277 from patent US 6555339. SION AR308754 AR308754.1 GI:31700283 RDS UNKNOWN. ANISM UNKNOWN. Unclassified. I (bases 1 to 2724) HORS Liaw, CW., Behan, D.P. and Chalmers, D.T. LE Non-endogenous, constitutively activated human protein-cou	receptors JOURNAL Patent: US 655339-A 277 29-APR-2003; FEATURES Location/Qualiflers Bource Locatism="unknown" /mol_type="genomic DNA" Alignment Scores: 0 Length: 2724	11arity: 820.00 Matches: 9 51milarity: 99.78\$ Conservative: 0 51milarity: 99.78\$ Mismatches: 1 6 Gaps: 6 36-84 (1-907) x AR308754 (1-2724)	Oy 1 Met AspThrSerArgLeuGlyValLeuLeuSerLeuProValLeuLeuGlnLeuAlaThr 20	41 GlubroAspGlyArgMetLeuLeuArgValAspCysSerAspLeuGlyLeuSerGluLeu	Qy 81 LeuleuProAsnProLeuProScrLeuMrgPheLeuGluGluLeuArgLeuAlaGlyAsn 100 1	361 CTGCAGAATAATCAGCTAAGACACCACAGAAGCTCTGCAGAATTTGCGAAGCCTT 141 GlnSerLeuArgLeuAspAlaAsnHisileSerTyrValProProSerCysPheSerGly 141 GlnSerCcTGCGTCTGGATGCTAACCACATCAGCTATGTGCCCCCCAAGCTGTTCAGTGGC 121 CAATCCCTGCGTCTGGATGCTAACCACATCAGCTATGTGCCCCCCAAGCTGTTTCAGTGGC 161 LeuHisSerLeuArgHisLeuTrpLeuAspAspAsnAlaLeuThrGluIleProValGln

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NRTHELGEKKCFDGLHSLETLDLNYNUNLDEFPTARTRILSKUEZLGFFBNNIRSIPERA
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ARHGAMWENGVGCHVIGFLSIFASESSVFLLTLAALERGFSVKYSAAFETKAPFSSLK
VIILLCALLALTWAAVPLLGGSKYGASPLCLPDPFGEBSTWGYNVALLILLNSLCFLMM
VIATKLYCALDLGGGLGANTGALLATALLLTACTLACPVAFLSFSSLINLTFISP
EVIKFTLYVVVPLAGGLNPLLYIFNHFKEDLVSLRGCTYVWTRSKHPSLMSINSDD
VEKQSCDSTQALVTFTSSITYDLPPSSVPSPAYPVTESCHLSSVAFVPCL"
                                                                                                                                               o mRNA linear PRI 17-NOV-1998
receptor LGR5 (LGR5) mRNA, complete
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RMLLRVDCSDLGLSELPSNLSVFTSYLDLSMNNISQLLPNPLPSLHFLEELRLAGNAL
TYIPKGAFTGLYSLKVLMLQNNQLRHVPTEALQNLRSLQSLRLDANHISYVPPSCFSG
                                                                                                                                                                                                                                                                                                                                                                               Heu, S.Y., Liang, S.G. and Hsueh, A.J.
Characterization of two LGR genes homologous to gonadotropin and thyrotropin receptors with extracellular leucine-rich repeats and G protein-coupled, seven-transmembrane region
Mol. Endocrinol. 12 (12), 1830-1845 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor; similar to glycoprotein hormone receptors; similar to FSH receptor, LH receptor and TSH receptor"
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Catarrhini; Hominidae; Homo
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    protein id="AAC77911.1"
    db_xref="GI:3885472"
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Hsu,S.Y., Liang,S.G. and Hsueh,A.J.W.
Direct Submission
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Gaps:
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/mol_type="mRNA"
/db_xref="taxon:9606"
1. .2724
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Dr., Stanford, CA 95305-5317, USA
Location/Qualifiers
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G protein-coupled 1
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Mammalia; Butheria; Primates;
                                          2700 TGTGGCATTTGTCCCATGTCTC 2721
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                    rValAlaPheValProCysLeu
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/gene="LGR5"-
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        uProProSerSerValProSerProAlaTyrProValThrGluSerCysHisLeuSerSe
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1861 TTTGGCAGCTTTGCACGACATGGTGCTGGTGGAGAATGGGGTTGCCATGTCATT
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                                                                 TGTTCACCTTCCCCAGGCCCCTTCAAACCCTGTGAACACCTGCTTGATGGCTGGATC
                                                                                                                                                                                                              ThrvalPheArgSerProLeuTyrIleSerProIleLysLeuLeuIleGlyValIleAla
                                                                                                                                                                                                                                             1741 ACAGTTTTCAGATCCCCTCTGTACATTTCCCCCCATTAAACTGTTAATTGGGGTCATCGCA
                                                                                                                                                                                                                                                                                                                                PheGlySerPheAlaArgHisGlyAlaTrpTrpGluAsnGlyValGlyCysHisValIle
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                                          CysSerProSerProGlyProPheLysProCysGluHisLeuLeuAspGlyTrpLeuIle
                                                                                                                             ArgileGlyValTrpThrIleAlaValLeuAlaLeuThrCysAsnAlaLeuValThrSer
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FT / Organism='Homo sapiens (human)'. FEATURES Location/Qualifiers 12082 / organism="Homo sapiens" / mol_type="genomic DNA" / db_xref="taxon:9606"	0 Length: 606.00 Matches: 7: 99.71% Conservat	ty: 99.71% Mismatches: 66.81% Indels: 6 Gaps: -907) x BD135244 (1-2082)	215 Leuhi sLeuhi sAsnAsnArgilehi sSerLeuGlyLysLysCysPheAspGlyLeuhi s	235 Serleugluthirleudaghteudaghtyraghashleudaghglurherrothralailearg	255 ThreewsersenteurysGlubewolyphenisSersensensenieArgserileFroGlu 121 ACHT[275 LygalaPhevalGlyAsnbroSeleullefnrileHisPheryrappasnbrolleGin 181 AadcalTTGTAGGCACCTTCTCTTATTACAATACATTCTATGACAATCCCAACCAA	Oy 295 PneValCIYArgSerAlaPneGlnH18LeuProGluLeuArgInLeuAffnLFeuThTLeuAffnLY 314	Oy 315 AlaSerGlnIleThrGluPheProAspLeuThrGlyThrAlaAsnLeuGluSerLeuThr 334	Qy 335 LeuThrGlyAlaGlnIleSerSerLeuProGlnThrValCysAsnGlnLeuProAsnLeu 354	Oy 355 GlnValLeuAspLeuSerTyrAsnLeuLeuGluAspLeuProSerPheSerValCysGln 374	Oy 375 LysLeuGlnLysleAspLeukrgHisAsnGlulleTyrGlulleLysValAspThrPhe 394	395 GlnGlnLeuLeuSerLeuArgSerLeuAsnLeuAlaTrpAsnLyslleAlalleIleHis	Qy 415 ProAsnAlaPheSerThrLeuProSerLeuIleLysLeuAspLeuSerSerAsnLeuLeu 434	Oy 435 SerSerPheProlleThrGlyLeuthisGlyLeuThrHisLeuLysLeuThrGlyAsnHis 454	Qy 455 AlaLeuGlnSerLeu-IleSerSerGluAsnPheProGluLeuLysVallleGluWet.Pr 474	Qy 474 OTYTALATYTGINCYSCYSALAPHEGIYVAICYSGIUASNALATYTLYSILESSETASNGI 494
	Oy 760 rpAspCysSerMetValLysHisIleAlaLeuLeuLeuPheThrAsnCysIleLeuAsnC 780	Db 2339 GCCCTGTGGCTTTCTTGTCCTTCTCTTAATAAACCTTACATTTATCAGTCCTGAAG 2398 Qy 800 allleLysPhelleLeuLeuValValProLeuProAlaCysLeuAsnProLeuLeuT 820	Db 2399 TAATTAAGTTTATCCTTCTGGTAGTCCCACTTCCTGCATGTCTCAATCCCTTCTCT 2458 Qy	Qy 840 alTrpThrArgSerLysHisProSerLeuWetSerlleAsnSerAspAspValGluLysG 860 Db 2519 TCTGGACAAGATCAAAACACCCCAAGCTTGATGTCAATTAACTCTGATGATGTGGAAAAAC 2578	Qy 860 InSerCysAspSerThrGlnAlaLeuValThrPheThrSerSerSerIleThrTyrAspL 880	Qy 880 euProProSerSerValProSerProAlaTyrProValThrGluSerCysHisLeuSerS 900	Oy 900 erValalaPheValProCysLeu 907 	SULT 11 135244	BD135244 ON BD135244		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 2082)	Novel mammalian G protein-coupled receptor h leucine-rich repeating domain Patent: JP 2002507406-A 2 12-MAR-2002; THE BOARD OF TRUSTEES OF THE LELAND STANFORD		U, SHAN GUANG LIANG, PETRUS	PC C12N1/219, A01K67/027, C07K14/705, C07KL6/28, C12N1/15, C12N1/19, PC C12N1/21, C12N	extracellular CC leucine-rich repeating domain FH Key Location/Qualifiers FT source 12082

Qy 854 rAspAspVi Db 1920 rGarGarGr Qy 874 rSerlleri Db 1980 CAGCARCA	894	RESULT 12 AC078860/c LOCUS AC078860 DEFINITION Homo sapies		ORGANISM Homo sapier ORGANISM Bukaryota; Mammalia;)	AUTHORS Muzny, D.M. Authors Alsbrooks,	Burch, P., J Carter, M., Carter, M.,	Davy-Carro, Davy-Carro, Denn, A.L., Dugan-Roch	Flagg, N., Garcia, A., Garcia,	Hodgson, A. Howard, S., Howard, S., Jacobson, B	Kraitsoun, B Kratovic, J Lewis, L., J Loulseged, J	Marindale Mador,M., Miner,Z., I	Nguyen, Nguyen, Nguyen, Oguh, M., Ol	CULLES, N., RUIZ, S., S. Shooshtari Stanley, H.	Thomas, N., Vinson, R., Washington	TITLE Direct Sub JOURNAL Unpublishe	AUTHORS Worley K.C AUTHORS Worley K.C TITLE Direct Sub- JOURNAL Submitted of Molecul.
494 nTrpAsnLysGlyAspAsnSerSerMetAspAspLeuHisLysLysAspAlaGlyMetPh 514	Greaccireaad IncysserProse 	uLeudepGlyTrpLeulleArglleGlyValTrpThrIleAlaValLeudlaLeuThrCy	574 GABRABLALOUVALThrSerThrValPheArgSerProLouTyrIleSerProIleLygLe 594	594 uleulledlyVallleAlaAlaValAsnWetLeuThrGlyValSerSerAlaValLeuAl 614 	614 aGlyValAspAlaPheThrPheGlySerPheAlaArgHisGlyAlaTrpTrpGluAsnGl 634 	634 yValGlyCysHisVall1eGlyPheLeuSerIlePheAlaSerGluSerSerValPheLe 654	654 uleuThrleuAlaAlaLeuGluArgGlyPheSerVallysTyrSerAlaLysPheGluTh 674 	674 rlysalapropheserSerieulysValllelleLeuLeuCysAlaLeuLeuAlaLeuTh 694 	694 rMetalaalavalProLeuLeuGlyGlySerLysTyrGlyalaSerProLeuCysLeuPr 714 	714 oLeuProPheGlyGluProSerThrMetGlyTyrMetValAlaLeuIleLeuLeuAsnSe 734	734 rLeuCysPheLeuMetMetThrIlealaTyrThrLysLeuTyrCysAsnLeuAspLysG1 754	754 yAspLeuGluAsnIleTxpAspCysSerMetValLysHisIleAlaLeuLeuLeuPheTh 774 	774 TABRCYBILELEUABRCYSProValAlaPheLeuSerPheSerSerLeuIleABrLeuTh 794	794 rPhelleSerProGluVallle!ysPhelleLeuLeuValValValProLeuProAlaCy 814	814 sLeudsnProLeuleuTyrIleLeuPheAsnProHisPheLysGluAspLeuValSerLe 834 	834 uArglysGlnThrTyrValTrpThrArgSerLysHisProSerLeuMetSerIleasnSe 854
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Libi, Rutherial, Findaces; Catarinin; Hominidae; Homo.

"D.M., Adams,C., Adio-Oduola,B., All-Ceman,F.K., Allen,C.,

"Ooks,S.L., Amaratumage,H.C., Are.J.R., Banks,T., Barbaria,J.,

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"A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,M.,

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"A., Garner,D., Hulyk,S., Hume,J., Harris,C., Harris,K.,

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"A., Mulyk,P., Hanson,R., Jolivet,S., Joudah,S.,

"A., Martinez,B., Mason,B., Marondel,I., Martin,R., Luna,R.,

"Maheshwari,M., Mapua,P., Marondel,I., Martin,R., Luna,R.,

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"A., Martinez,B., Mercher,B., Socott,G., Shen,H., Stone,H., Sutco,H., Sutco,R., Taylor,T., Warren,R.,

"Martinez,B., Warren,R., Warren,R., Warren,R., Mulle,R., Warten,R., Warren,R., Warr 145165 bp DNA linear PRI 23-JAN-2003 ens 12 BAC RP11-186F10 (Roswell Park Cancer Institute Library) complete sequence. ValGluLyBGlnSerCyBABDSerThrGlnAlaLeuValThrPheThrSerSe 874 ThrTyrAspLeuProProSerSerValProSerProAlaTyrProValThrGl 894 , Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Eutheria, Primates, Catarrhini, Hominidae, Homo. 19 GI:13491193 1 to 145165) ens (human)

Direct Submission Submitted (07-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One

TITLE JOURNAL

AUTHORS

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COMMENT

AUTHORS

REFERENCE

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tcatgaccta (a) tcatgaccat
ctatctctac (g) aaagaaaaga
aatgacttat (a) aaatggacc
cttadactgt (g) aatggtaagg
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agaagggtgt (g) gacattaata
acatggtgtt (g) cacttaata
aaatatgtc (c) taaataaagt
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                                                                                                   agatgtggat (g)gctgtggctt
tttcggctca (c)tgcaacctcc
aaaacaacat (a)caatagataa
                                                                                                                                                                                                    atcgttattg(t)tgttaatttt
ttttttattt(t)tatagttaat
                                                                                                                                                                               ttgtattgca (a) atggcatctt
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complement(6. .223)
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                                                                           Edited+Context
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ettagaete (n) apagecoc
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getaatete (n) optetetage
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tttcggctca (n) tgcaacctcc
aaaacaacat (n) caatagataa
ttgtattgca (n) atggcatctt
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gcatggtgtn (n) ncacttaata
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gcttacacta (n) aaaatgaacc
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complement (2152. .2449)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consenues splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                      Direct Submission
Submitted (31-MAR-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 145165)
                                                                                                                                                                                                                                                                                                                                                                                                Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 6 (bases 1 to 145165)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submits (12-JAN-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Max 31, 2001 this sequence version replaced gi:13324671.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.
                                                                                                                                                                                                                                                   Submitted (01-APR-2001) Human Genome Sequencing Center, Department of Moldular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 145165)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145169
TX 77030, USA
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Baylor Plaza, Houston,
3 (bases 1 to 145165)
                                                                                                                                                                                                                                                                                                                                                 Worley, K.C.
Direct Submission
                                                                                                                                                                                                                           Direct Submission
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                                               Worley, K.C.
                                                                                                                                                                                            Worley, K.C.
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40

145165 362 0

Length: Matches: Conservative:

0 362.00 100.00%

Percent Similarity:

Score:

144455 5.28339e-05 0.0137759 19

Phrap values in estimate:
Average error rate (BCM-Phrap estimate):
Fraction of Phrap values less than 40:
Number of consensus changing edits:
Number of N's in consensus:

Alignment Scores: Pred. No.:

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L Unpublished

E. Cases 1 to 4095)

S. Saogai, T. and Yamamoto, J.

Direct Submission

L. Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute,

Genomics Laborstory, 1332-3 Yama, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:gl-438-52-3975, Fax:81-438-52-386)

HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass
sequencing, clone selection and full insert sequencing; Helix
Research Institute (supported by Japan Key Technology Center etc.);

cDNA library construction: Institute of Medical Science, University

of Tokyo, Laboratory of Genome Structure, Human Genome Center.
                AK075399 4095 bp mRNA linear PRI 03-SEP-2002 Homo sapiens cDNA PSEC0089 fis, clone PLACE1001148, highly similar to Homo sapiens orphan G protein-coupled receptor HG38 mRNA.
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/note="This 284 bases segment is not present in AF062006
and AF061444, probably caused by alternative splicing"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T.,
Nakamura,Y., Sato,H., Nagahari,K., Sugano,S. and Isogai,T.
HRI human cDNA sequencing project
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/clone_Tib="ptacenta"
/noce="cloning vector: pME18SFL3"
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Homo sapiens (human)
Homo sapiens
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Mismatches:
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Matches:
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SP-1998 EP 98203213.8
YUDEISU CHRISTINA HEIKOPU, PETORIYUSU JOHANNES VAN DEL SUPEKKU
CIZNIS/09,A61K38/00,A61P15/08,A61P43/00,C07K14/72,C1ZN1/15, PC
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PC C12N1/19,
PC C12N1/21,
C12X1/19,
PC C12N1/21,
C12N1/21,
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C12N1/21,
C12N1/20,
C12N1/2
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/organism='Unidentified'
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
Novel gonadotropin receptor
Patent: JP 2000125884-A 3 09-MAY-2000;
PACO NOBEL WO CO Unidentified
PN JP 2000125884-A/3
PD 09-MAY-2000
PF 05-FEB-1999 JP 1999029120
PR 06-FEB-1998 EP 98203257.6,27-JUL-1
PI YUDELGU CHRISTINA HEIKOPU, PETORIYUSU
PC CILMIS/09,A61K38/00,A61P15/08,A61P43
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Novel gonadotropin receptor.
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B42915. GT:18627551
JP 2000125884-A/3.
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Heikopu,Y.C. and Supekku,P.J.V.D.
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Search completed: July 12, 2005, 11:03:53 Job time : 10120 secs
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Matches:
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Gaps:
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    .606
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

                                                                                                                                                                 Heikoop,J.C. and Van Der Spek,P.J.
Gonadotropin receptor
Patent: EP 0950711-A 3 20-OCT-1999;
AKZO NOBEL NV (NL)
Location/Qualifiers
                                                                                   AX016185 606 bp
Sequence 3 from Patent EP0950711.
AX016185
AX016185.1 GI:10041794
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27, Appl 1, Appli 17399, A 17397, A 16001, A

21653, A 842, App 3399, Ap

16682, Ā 78, Appl 62035, A

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2369, Ap 6371, Ap

Perfect score:

Sequence:

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Scoring table:

Word size:

Searched:

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Sequence 263, Application US/09170496D

Batent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Receptors
FILE REFERENCE: ARRA-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 263
                                                                                                                                                                                                                Sequence 25920, A
Sequence 3670, Ap
Sequence 6300, Ap
Sequence 22246, Ap
Sequence 9010, Ap
Sequence 7526, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 16704, A
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US-08-817-345-1
US-08-949-016-17399
US-09-949-016-17399
US-09-949-016-17399
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US-09-513-999C-310
US-09-513-999C-310
US-09-513-998-310
US-09-621-976-682
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US-09-949-016-79941
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US-09-170-496D-263
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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/Cgn2_1/USPTO_spool/US10751736/runat_12072005_083642_22200/app_query.fasta_1.1095
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-LOOPEXT=0 -UNITS=5its -START=1 -END=-1 -MATRIX=01igo -TRANS=human40.cdi
-USTE45 -DOCALIGN=200 -THR SCOREA=quality -TRR MINL=1 -ALIGN=15 -MODE=LOCAL
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-NO_WMAP -LAARGEQUERY -NEG SCORES=0 -WAIT -DSPBELOKE=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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                      322 GGGGGGGGCTCTCCCAGGTCTGGTGTTGCTGAGGGGGCTGCCCCACACACTGTCATTGC
                                            GluProAspGlyArgMetLeuLeuArgValAspCysSerAspLeuGlyLeuSerGluLeu
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41 GlubroAspGlyArgMetLeuLeuArgValAspCysSerAspLeuGlyLeuSerGluLeu 60	121 LeuGlnAsnAsnGlnLeuArgHisValProThrGlualaLeuGlnAsnLeuArgSerLeu	GCTTTAGAAGTTTATCGCATGCAAGCCATGACCTGGCCCTGAACAAATACACCAC 600 11eProAspTyralaPheGlyAsnLeuSerSerLeuValValLeuHisLeuHisAsnAsn 220	THAATTACAATAACCTTGATGAATTCCCCACTGCAATTAGGACATCTCCAACCTTAAA 780 GluleuGlyPheHisSerAsnbaATTCCCCACTGCAATTAGGACATCTCCTAACCTTAAA 780 GLAACTAGGATTTCATAGCAACAATAATCAGGTCGATACCTGAGAAAGCATTTGTAGGCAAC 840 ProSerLeuIleThrIleHisPheTyrAspAsnProIleGlnPheValGlyArgSerAla 300	TGAA 960 nile 340

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                                                                                                      LeuSerIlePheAlaSerGluSerSerValPheLeuLeuThrLeuAlaAlaLeuGluArg
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APPLICANT: Tang, Y Tom
APPLICANT: Tang, Y Tom
APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Rang, Jian-Rui
APPLICANT: Tang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Yamazaki, Victoria
APPLICANT: Tamazaki, Victoria
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Ronghong
APPLICANT: Wang, Ponghong
APPLICANT: Wang, Ponghong
APPLICANT: Wang, Nonghong
APPLICANT: Wenran, Tom
APPLICANT: Wenran, Tom
APPLICANT: Wenran, Ponghong
APPLICANT: Softh Pungare 2001-03-05
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SEQ ID NO 7:29
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Patent No. 6783969
GENERAL INFORMATION:
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APPLICANT: Guegler, Karl, J.

TILE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED
FILE REFERENCE: PA-0113 US
CURRENT APPLICATION NUMBER: US/09/495,050A
CURRENT APPLICATION NUMBER: 60/118,318
PRIOR FILING DATE: February 1, 1999
NUMBER OF SEQ ID NOS: 305
SOFTWARE: PROGram
SEQ ID NO 220
LENGTH: 723
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                                                                          CCCTGTGGCTTTCTTGTCCTTCTCCTTTAATAAACCTTACATTTATCAGTCCTGAAGT
                                                                                                                                          rlleLeuPheAsnProHisPheLysGluAspLeuValSerLeuArgLysGlnThrTyrVa
                                                                                                                                                                                                                                                                                                                              nSerCygAspSerThrGlnAlaLeuValThrPheThrSerSerSerIleThrTyrAspLe
                                                     sProValAlaPheLeuSerPheSerSerLeuIleAsnLeuThrPheIleSerProGluVa
                                                                                                                          800 lileLysPhelleLeuValValValValProLeuProAlaCysLeuAsnProLeuLeuTy
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                                                                                                                                                                                                                                                             840 lTrpThrArgSerLysHisProSerLeuMetSerIleAsnSerAspAspValGluLysGl
                                                                                                                                                                                                                                                                                                                                                              2580 GTCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTTATGACCT
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US-09-495-050A-220
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Mismatches:
Indels:
Gaps:
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Matches:
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US-09-495-050A-220
Sequence 220, Application US/09495050A
Patent No. 6492505
GENERAL INFORMATION:
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FEATURE:
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Best Local Similarity:
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Pred. No.:
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Sequence 1, Application US/09153593A

Sequence 1, Application US/09153593A

GENERAL INFORMATION:

APPLICANT: ELICHORRAGY, NABIL A

APPLICANT: ELICHORRAGY, NABIL A

TILLE OF INVENTION: NOVEL 7TM RECEPTOR (H2CAA71)

FILE REFERENCE: GH-70055-1

CURRENT APPLICATION NUMBER: US/09/153,593A

CORRENT FILING DATE: 1999-09-15

EARLIER APPLICATION NUMBER: 08/866,757

EARLIER FILING DATE: 1997-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
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                                                                                                                                 OCREVIER: 15M COMPACTOR.
OPERATING SYSTEM: DOS
SOFTWARE: FRASEQ for Windows Version 2.0
CURRENT PAPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY, AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
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Mismatches:
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEPAX: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 846169
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4203 base pairs
                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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Best Local Similarity:
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Pred. No.:
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US-09-153-593-1
                                         COUNTRY:
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Batent No. 6492505
GENERAL INFORMATION:
APPLICANT: Roopa, Reddy
APPLICANT: Guegler, Karl, J.
APPLICANT: Au-Young, Janica
ITILE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED ITILE REFERENCE: PA-0013 US
FILE REPERENCE: PA-0013 US
CURRENT PILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 6/118 318
PRIOR PLICATION NUMBER: 6/118 318
PRIOR PLICATION NUMBER: 9/1199
NUMBER OF SEQ ID NOS: 305
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                              285 ThrileHisPheTyrAspAsnProlleGlnPheValGlyArgSerAlaPheGln 302
                                                                                                                                                                                                                                                                                                                                                                                     436 ACCATACACTITITATGATAACCCAATCCAGTITGTGGGAAGATCGGCATTCCAG 489
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COTHER INFORMATION: Incyte ID No. 6492505 2470285CT1

US-09-495-050A-214
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APPLICANT: ELSHOURBAGY, NABIL A
APPLICANT: LI, XIAOTONG
APPLICANT: BERGAM, DENK J
TITLE OF INVENTION: NOVEL 7TM RECEPTOR (H2CAA71)
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-751-736-84 (1-907) x US-09-495-050A-214 (1-2612)
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Matches:
Conservative:
Mismatches:
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Mismatches:
Indels:
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Patent No. 5858716
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TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Query Match:
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                                         ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...
US-09-799-451-723
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US-09-495-050A-214
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Pred. No.:
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LENGTH: 2612
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US-09-556-916-25
; Sequence 25, Application US/09556916
; Patent No. 6548271
; GENERAL INFORMATION:
; APPLICANT: Turner, Alex
; APPLICANT: Turner, Alex
; APPLICANT: Turner, Alex
; APPLICANT: Triadbraich, Glenn
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6548271el Human Transporter Proteins
; FILE REFRENCE: 8535-041-999
; CURRENT APPLICATION NUMBER: US/09/556,916
; CURRENT FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 2019
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US-09-397-787-240

| Sequence 240, Application US/09397787
| Patent NO. 6468758
| GENERAL INFORMATION:
| APPLICANT: Benson, Darin R. |
| APPLICANT: Mitcham, Jennifer L. |
| TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS |
| FILE REPERBENCE: 21012.1466C2 |
| CURRENT APPLICATION NUMBER: US/09/397,787 |
| CURRENT APPLICATION NUMBER: US/09/397,787 |
| SEQ ID NO 240 |
| LENGTH: 453 |
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         Mismatches:
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Best Local Similarity: 100.00%
Query Match: 1.43%
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US-09-556-916-25
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US-09-397-787-240
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Best Local Similarity:
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Pred. No.:
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPREBUCE: CL001307
CURRENT APPLICATION NUMBER: 06/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTHARE: REALESEQ for Windows Version 4.0
LENGTH: 2680
                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Turner, Alex
APPLICANT: Zambrowicz, Brian
APPLICANT: Sandrowicz, Brian
APPLICANT: Nehle, Michael
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6548271el Human Transporter Proteins
FILE REFERENCE: 8535-041-999
CURRENT APPLICATION NUMBER: US/09/556,916
CURRENT FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 27
LENGTH: 2019
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                                                         US-10-751-736-84 (1-907) x US-09-556-916-25 (1-2019)
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; Patent No. 6812339
                                                                                                                                                                                                             Sequence 27, Application US/09556916
Patent No. 6548271
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9.00
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US-09-556-916-27
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Best Local Similarity:
Query Match:
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US-09-949-016-5657
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Pred. No.:
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APPLICANT: Strabla, Timothy
APPLICANT: Strabla, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ghosh, Reena
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6783969el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REPERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT PILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOPTHARE: PP_FL_genes Version 2.0
SEQ ID NO 422
LENGTH: 2820
                                                                                                 US-10-751-736-84 (1-907) x US-09-949-016-5657 (1-2680)
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Matches:
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                                                                                                                                                                                                                                           Sequence 422, Application US/09799451
Patent No. 6783969
GENERAL INFORMATION:
APPLICANT: Tang, V. Tom
APPLICANT: Goodrich, Ryle
APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Asungi, Jie
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Wang, Zhiwei
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; Sequence 458, Application US/10101464A
; Patent No. 6768041
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; LOCATION: (265)..(2577)
US-09-799-451-422
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ORGANISM: Homo sapiens
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APPLICANT: Strabala,
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and Their Use in the Modification of Plant Cell Signaling
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Sequence 1, Application US/07792865D
Sequence 1, Application US/07792865D
Patent No. 56462T)
GENERAL INFORMATION:
APPLICANT: John W. Barnwell, Mary W. Galinski,
APPLICANT: Samuel P. Wertheimer
TITLE OF INVENTION: THE APLCAL END OF THE PARASITE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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Mismatches:
Indels:
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           354 LeuGlnValLeuAspLeuSerTyrAsn 362
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MEDIUM TYPE: Diskette, 5.25 inch, 360
COMPUTER: IBM or IBM-compatible
OPERATING SYSTEM:
POPEMATING SYSTEM:
CORPUTER: USPONS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/792,865D
FILING DATE: 19911004
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: PCT/US90/01849
FILING DATE: APPLICATION:
APPLICATION NUMBER: PCT/US90/01849
FILING DATE: APPLICATION:
APPLICATION NUMBER: 34,354
REFERENCE/DOCKET NUMBER: 5986/14692-U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                598 CTTCAGGTTCTCGACCTGTCTTATAAT 624
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STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
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TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
DESCRIPTION:
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRACHENT TYPE:
ORGANISM: P.vivax
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
CELL TYPE:
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CHROMOSOMES/SEGMENT:
MAP POSITION:
HAPLOTYPE:
NAME/KEY:
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TIDENTIFICATION METHOD:
OTHER INFORMATION: Figure 1A (sheets 1-4) in the
OTHER INFORMATION: application, as filed.
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JOURNAL:

JOURNAL:

VOLUME:

SESUE:

DATE:

DOCUMENT NUMBER:

FILING DATE:

FILING DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-07-792-865D-1
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Percent Similarity: 1
Best Local Similarity: 1
Query Match: 1
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Search completed: July 12, 2005, 13:02:23 Job time : 436 secs

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July 12, 2005, 07:34:33; Search time 33 Seconds (without alignments) 2051.718 Million cell updates/sec
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: /cgn2 6/ptodata1/liaa/5B_COMB.pep:*
: /cgn2 6/ptodata1/liaa/6A_COMB.pep:*
: /cgn2 6/ptodata1/liaa/6A_COMB.pep:*
: /cgn2 6/ptodata1/liaa/RB_COMB.pep:*
: /cgn2 6/ptodata1/liaa/PCTUS_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                      OM protein - protein search, using sw model
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length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

Sequence 278, App Sequence 2, Appli Sequence 2, Appli Sequence 6, Appli Sequence 6, Appli Sequence 2, Appli GENERAL INFORMA Sequence 264, App Sequence 61, Sequence 5, Apsequence 5, Apseq Description Sequence Sequence S Sequence Sequence Sequence Sequence -09-170-496D-264 -09-170-496D-278 -08-866-757-2 S-07-757-342D-6 S-09-461-657B-6 S-08-487-886-2 S-08-482-855-2 S-08-474-986-2 S-07-714-453A-61 S-07-757-342D-5 5.09-826-509-587 5-07-741-453A-59 5-09-826-509-403 5-07-741-453A-54 5-07-757-342D-3 -09-826-509-399 -09-826-509-407 -09-826-509-395 -09-826-509-415 -09-153-593-2 -07-757-342D-(Length Query Match 4696 1217.5 1217.5 1217.5 621.5 621.5 621.5 591.5 592.5 593.6 593. Result No. 202221098743211098765 202221098767321098765

300 360 301 FQHLPELRTUTLNGASQITEFPDLTGTANLESLTLTGAQISSLPQTVCNQLPNLQVLDLS 360 YNLLEDLPSFSVCQKLQKIDLRHNEIYEIKVDTFQQLLSLRSLNLAWNKIAIIHPNAFST 420

361

Sequence Sequence Sequence

US-09-461-657B-4 US-09-826-509-423

Sequence

Seguence

-826-509-411 -826-509-419

301

POHLPELRTLTLNGASQITEFPDLTGTANLESLTLTGAQISSLPQTVCNQLPNLQVLDLS

241 LAYANILDEFPTAIRTLSNLKELGFHSNNIRSIPEKAFVGNPSLITIHFYDNPIQFVGRSA

LNYNNLDEFPTAIRTLSNLKELGFHSNNIRSIPEKAFVGNPSLITIHFYDNPIQFVGRSA

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              LQNNQLRHVPTEALQNLRSLQSLRLDANH1SYVPPSCFSGLHSLRHLMLDDNALTEIPVQ
                                                                                                       241 INYNNLDEFPTAIRTLSNLKELGFHSNNIRSIPEKAFVGRPSLITIHFYDNPIQFVGRSA
                                                                                                                                                                                 LONNOLRHVPTEALONLRSLOSLRLDANHISYVPPSCFSGLHSLRHLWLDDNALTEIPVQ
                                                          AFRSLSALQAMTLALNKIHHI PDYAFGNLSSLVVLHLHNNRIHSLGKKCFDGLHSLETLD
                                                                                          LINYNNLDEFPTAIRTLSNLKELGFHSINITRSIPEKAFVGNPSLITIHFYDNPIQFVGRSA
                                                                                                                                        FOHLPELRILILINGASQITEFPDLTGTANLESLTLTGAQISSLPQTVCNQLPNLQVLDLS
                                                                                                                                                  CSPSPGPFKPCEHLLDGWLIRIGVWTIAVLALTCNALVTSTVFRSPLYISPIKLLIGVIA
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                                                                                                                                                                                                                                 LPSLIKLDLSSNLLSSFPITGLHGLTHLKLTGNHALQSLISSENFPELKVIEMPYAYQCC
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Patent No. 5858716
GENERAL INFORMATION:
APPLICANT: ELSHOURBAGY, NABIL A
APPLICANT: ELSHOURBAGY, NABIL A
APPLICANT: ELSHOURBAGY, NOVEL 7TITLE OF INVENTION:
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
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STATE: PA
COUNTRY: US
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US-08-866-757-2
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Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT APPLICATION NUMBER: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.9%;
Matches 906; Conservative
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CORGANISM: Homo sapiens
US-09-170-496D-278
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US-09-170-496D-278
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LENGTH: 907
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RESULT 5
US-07-757-342D-6
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ZIP: 19482

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: DISKETTE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,757
FILING DATE: 30-MAY-1997
CLASSIFICATION NATA: APPLICATION NUMBER: RILING DATE:
APPLICATION NUMBER: ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REGISTRATION NUMBER: CH-70055
TELEFONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 25.9%; Score 1217.5; DB Best Local Similarity 46.3%; Pred. No. 6.1e-89; Matches 250; Conservative 88; Mismatches 183
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INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 644 amino acids
                                                                                                                                                                                                                                                                           610-407-0701
                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 644;
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88; Mismatches 183; Indels
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Patent No. 6218509
GENERAL INFORMATION:
APPLICANT: IGARASHI, Masao
NANEGISHI, Takashi
NAKAMURA, Kazuto
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
                                         GENERAL INCORNATION:
APPLICANT: ELSHOURBAGY, NABIL A
APPLICANT: ELSHOURBAGY, NABIL A
APPLICANT: BERGSWA, DERK J
TITLE OF INVERTION: NOVEL 7TM RECEPTOR (H2CAA71)
FILE REFERENCE: GH-70055-1
CURRENT PAPLICATION NUMBER: US/09/153,593A
CURRENT PILING DATE: 1998-09-15
BARLIER APPLICATION NUMBER: 08/866,757
BARLIER PILING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FABELSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.9%; Score 1217.5; 46.3%; Pred. No. 6.1e
Sequence 2, Application US/09153593A
Patent No. 6174994
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 46.3%
Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: HOMO SAPIENS
US-09-153-593-2
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705

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340 VVD------VTCSPKPDAFNPCEDIMGYNILRVLIWFISILAITGNTTVLVVLTTS 389
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APPLICANT: MINEGISHI, TAKASHI
APPLICANT: NAKAMURA, KAZUTO
TITLE OF INVENTION: NUCLEIC ACID MOLECULARES ENCODING HUMAN LUTEINIZING
TITLE OF INVENTION: HORMONE-HUMAN CHORIONIC GONADOTROPIN RECEPTOR PROTEIN
TITLE OF INVENTION: HORMONE-HUMAN CHORIONIC GONADOTROPIN RECEPTOR PROTEIN
TITLE OF INVENTION: AND TRANSFORMANTS THEREOF
CURRENT APPLICATION NUMBER: US/09/461,657B
CURRENT PILING DATE: 2002-04-16
PRIOR FILING DATE: 1991-09-10
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                                                                                        FASESSVFLLTLAALERGFSVKYSAKFETKAPFSSLKVIILLCALLALTMAAVPLLGGSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 KIQSLQKVLLDIQ-------DNINIHIVARNSFMGL
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US-09-461-657B-6
; Sequence 6, Application US/09461657B
; Patent No. 6635445
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SEQ ID NO 6
LENGTH: 692
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APPLICANT: IGARASHI, MASAO
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US-09-461-657B-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 692;
                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMENT Release #1.0, Version #1.25
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APPLICATION NUMBER: US/07/757,342D
FILING DATE: 10-Sep-1991
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 23.1%; Pred. No. 3.1e Matches 211; Conservative 129; Mismatches
                                                                                                                                                                                                                                                                                                                ATTOREY AGENT INFORMATION:
NAME: BUCKLEY, Linda M.
REGISTRATION NUMBER: 31003
REFERENCE/DOCKET NUMBER: 41226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-07-757-342D-6
                            STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 692 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                     STATE: Massachusetts
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CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/487,886 FILING DATE: 07-UNM-1995 CLASSIFICATION DATA: PRIOR APPLICATION DATA: FILING DATE: 15-MAR-1991 APPLICATION NUMBER: 07/670,085 FILING DATE: 15-MAR-1991 APPLICATION NUMBER: 07/670,085 FREGISTRATION NUMBER: 28846 REGISTRATION NUMBER: 28846 REGISTRATION NUMBER: US/252 TELEPHONE: (617) 723-1300 TELEPHONE: (617) 723-1300 TELEPHONE: (617) 723-1300 TELEPHONE: 695 TYPE: Amino acid TOPOLOGY: Linear MOLECULE TYPE: protein FEATURE: NAME/KEY: signal sequence LOCATION: -17 to -1 IDENTIFICATION METHOD: hydrophobic FEATURE:	NAME/KEY: putative amino-terminal extracellular domain COCATION: 1 to 349 IDENTIFICATION METHOD: similarity with other IDENTIFICATION METHOD: dimeric glycoprotein receptor extracellular IDENTIFICATION METHOD: domains, hydrophilic FEATURE: NAME/KEY: transmembrane domain IDENTIFICATION METHOD: similarity to other G IDENTIFICATION METHOD: similarity to other G IDENTIFICATION METHOD: protein-coupled receptor transmembrane domains	и и и и и и и и и и и и и и и и и и и	NAME/KEY: putative transmembrane region III COATION: 427 to 448 IDENTIFICATION METHOD: similarity to other G IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions, IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length NAME/KEY: putative transmembrane region IV LOCATION: 468 to 491 IDENTIFICATION METHOD: similarity to other G IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions, IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length	FEATURE: FASTURE: FASTURE:
	Db 390 QYKLTVPRFLMCNIAFADLCIGIYLLLIASVDIHYKSQYHNYAIDNQTGAGCDAAGFTV 449 Qy 646 FASESSVFLTLAALERGFSVKXSAKFETKAPFSSLKVIILLCALLALTWAAVPLLGGSK 705	Qy	2, 2 F. 57 FINFC FINFC ANT: ANT: ANT: ANT:	NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSEE: Ares-Gerono, Inc. ADRESSEE: Ares-Gerono, Inc. STREET: Exchange Place, 37th floor CITY: Boston STATE: MA COUNTRY: USA COUNTRY: USA COUNTRY: TEADABLE FORM: MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density COMPUTER: IBM PS/2, model 55 SX COMPUTER: MS-DOS version 4.0 SOPTWARE: VAX/VMS Mass11 via Kermit to IBM MS-DOS

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Amino acid
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STATE: MA
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NAME/KEY:
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                                                                                                                                                                                                                                                   protein-coupled receptor transmembrane regions, hydrophobic, about 20-23 amino acids in length
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                                                                                                                                                                                                   Gaps
                                                                                                                                                                Query Match 13.2%; Score 621.5; DB 1; Length 695; Best Local Similarity 22.4%; Pred. No. 4.5e-41; Matches 207; Conservative 146; Mismatches 306; Indels 265;
                                                                                 putative carboxy-terminal intracellular
                 other G
                 similarity to
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LOCATION: 592 to 613
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
                                                                                                                   614 to 678
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                                                                                                     domain
                                                                                                  ; NAME/KEY:
; LOCATION:
US-08-487-886-2
                                                                               NAME/KEY:
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similarity to other G
protein-coupled receptor transmembrane regions,
hydrophobic, about 20-23 amino acids in length
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protein-coupled receptor transmembrane domains
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1 to 349
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MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
COMPUTER: IBM PS/2, model 55.8X
COMPUTER: MS-DOS version 4.0
SOFTWARE: VAX/VMS_MSS11 via Kermit to IBM MS-DOS
                                                                                                                                                              Sequence 2, Application US/08482855
Patent No. 6121016
GENERAL INFORMATION:
APPLICANT: Kelton, Christie Ann
APPLICANT: Cheng, Shirley Vui Yen
APPLICANT: Nugent, No. 6121016een Patrice
TITLE OF INVENTION: Human Follicle Stimulating
TITLE OF INVENTION: Hormone Receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US/08/482,855 FILING DATE: 07-UN-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/670,085 FILING DATE: 15-WAR-1991 ATTORNEY/AGENT INFORMATION:
NAME: Williams, Stephan P. REGISTRATION NUMBER: 28546 REFERENCE/DOCKET NUMBER: US/252 TELECOMMUNICATION INFORMATION:
905
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Stephan P. Williams,
ADDRESSEE: Area-Serono, Inc.
STREET: Exchange Place, 37th floor
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IDENTIFICATION METHOD: hydrophobic
882 PSSVPSPAYPVTESCHLSSVAFVP
                                            668 RNGHCSSAPRVTNG---STYILVP
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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IDENTIFICATION METHOD:
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219 ANWRRQISELHPICNKS--ILRQEVDYMTQTRGQRSSLAEDN------ESSYSRGFDMT 329
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                                                                                                                                                                                                                                                      SPLYISPIKLLIGVIAAVNMLTGVSSAVLAGVDAFTFGSFARHGAWWENGVGCHVIGFLS 644
                                                                                                                                                                                                                                                                                                                                                                                                                       KYGASPLCLPLPFGEPSTMGYMVALILLNSLCFLMMTIAYTKLYCNLDKGDL-ENIWDCS 763
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                                                                                                                                                                     LLDFEEDL-KALHSVQCSPSPGPFKPCEHLLDGWLIRIGVWTIAVLALTCNALVTSTVFR
                                                                                                                                                                                                                                                                              423 SLIKLDLSSNLLSSFPITGLHGLTHLKLTGNHALQSLISSENFPELKVIEMPYAYQCCAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schweickhardt, Rene Lynn
Cheng, Shirley Vui Yen
Nugent, No. 6372711een Patrice
TITLE OF INVENTION: Human Follicle Stimulating
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REGISTRATION NUMBER: 28546
REFERENCE/DOCKET NUMBER: US/252
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APPLICATION NUMBER: 07/670,085
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GENERAL INFORMATION:
APPLICANT: Kelton, Christie Ann
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ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
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COUNTRY: USA
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protein-coupled receptor transmembrane regions,
hydrophobic, about 20-23 amino acids in length
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protein-coupled receptor
hydrophobic, about 20-23
                                                             protein-coupled receptor hydrophobic, about 20-23
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protein-coupled receptor
hydrophobic, about 20-23
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hydrophobic, about 20-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity to other G
                                             similarity to other G
                                                                                                                                                                     similarity to other G
                                                                                                                          NAME/KEY: putative transmembrane region III LOCATION: 427 to 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: putative transmembrane region VII
NAME/KEY: putative transmembrane region II LOCATION: 382 to 404
IDENTIFICATION METHOD: similarity to other IDENTIFICATION METHOD: protein-coupled receIDENTIFICATION METHOD: hydrophobic, about 2
                                                                                                                                                                                                                                                      NAME/KEY: putative transmembrane region IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transmembrane region VI
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                                                                                                                                             LOCATION: 427 to 448
IDENTIFICATION METHOD:
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IDENTIFICATION METHOD:
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IDENTIFICATION METHOD:
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LOCATION: 557 to 580
IDENTIFICATION METHOD:
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IDENTIFICATION METHOD:
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205 NLEELPN---
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                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
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                                                                                                                                                              SVFTSYLDLSMINISQLLPNPLPSIRFLEELRLAGNALTYIPKGAFTGLYSL-KVLMLQN 123
                                                                                                                                                                                                                  124 NOLRHVPTEALQNLRSIQSLRLD-ANHISYVPPSCFSGLHSLRHLWLDDNALTEIPVQAF 182
                                                                                                                                                                                                                                                                    RSLSALQAMTLALNKIHHIPDYAFGNLSSLVVLHLHNNRIHSLGKKCFDGLHSLETLDLN 242
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                                                                                                                                                                                                                                                                                                                                    DN------PESVILWINKNGIQ 183
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                                                                                                                8 VLLSLPVLLQLATGGSSPRSGVLLRGCPTHCH---CEPDGRMLLRVDCSDLGLSELPSNL 64
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                                                                                        Gaps
                                                                                       Matches 207; Conservative 146; Mismatches 306; Indels 265;
                                                               Length 695
                                                               DB 3;
                                                              13.2%; Score 621.5; DB 322.4%; Pred. No. 4.5e-41
TELEFAX: (617) 723-8923
LOCATION: 614 to 678
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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                                                                           Similarity
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US-08-474-986-2
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POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/741,453A
FILING DATE: 19911015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST
TELECPHONE: (202) 861-3000
TELEPHONE: (202) 822-0944
TELEX: 6714627 CUSH
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                                                                                                                                                                                                                                                                           CUSHMAN
; Sequence 61, Application US/07741453A; Patent No. 6228597; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 212; Conservative 152;
                                                                                                                                                                                                                                                                      SEE: CUSHMAN DARBY & 1615 L STREET, N.W. WASHINGTON, D.C.
                                                               APPLICANT: PARMENTIER, MARC
APPLICANT: LIBERT, FREDERIC
APPLICANT: DUMONT, JACQUES
APPLICANT: VASSART, GILBERT
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MEDIUM TYPE: Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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                                                                                                                                                         TITLE OF INVENTION: PITTLE OF INVENTION: AITLE OF INVENTION: ANUMBER OF SEQUENCES:
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STRANDEDNESS: Si
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64 LSVFTSYLDLSMNNISQLLPNPLPSLRFLEELRLAGNALTYIPKGAFTGLYSLKVLMLQN 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSVKYSAKFETKAPFSSLKVII----LLCALLALTMAAVPLLGGSKYGASPLCLPLPFGE 719
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                                                                                                                                                                                                                                                                                                                                                       Query Match 12.7%; Score 595; DB 3; Length 764;
Best Local Similarity 21.9%; Pred. No. 6.9e-39;
Matches 213; Conservative 148; Mismatches 301; Indels 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLOLVILLDLPRDLGGMGCSSP-----PCECHOEED----FRVTCKDI
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                                                          REFERENCE/DOCKET NUMBER: 41226
TELECOMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFRAX: (617)523-6440
                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-07-757-342D-5
                     NAME: BUCKLEY, Linda M.
REGISTRATION NUMBER: 31003
                                                                                                                                      TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 764 amino acids
TYPE: amino acid
ATTORNEY/AGENT INFORMATION
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                                                                                                    TL---PSLIKLDLSSNLLSSFPITGLHGLTHLKLTGNHALQSLISSENFPELKVIEMPYA 476
                                                                                                                              SHCCAFKNOKKIRGILESLMCNESSMOSLRORKSVNALNSPLHOEYEENLGDSIVGYKEK 340
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                                                                                                                                                                                                                                                                                                 SKPODTHNNAHYYVPFEEQEDEIIGFGQELKNPQEETLQAFDSHYDYTICGDSEDMVCTP
                                                                                                                                                                                                                                                                                                                                                                                 KSDEFNPCEDIMGYKFLRIVVWFVSLLALLGNVFVILLILLTSHYKLNVPRFLMCNLAFAD
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                   SYNLLEDLPSFSVCQKLQKIDLRHNBIYBIKVDTFQQLLSLRSLNLAMNKIAIIHPNAFS
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                                                                                                                                                                                    477 YQCCAFG-----VCENAYKISNQWNKGDNSSMDDLHK----
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: IGARASHI, MASAO
MINEGISHI, Takashi
NAKAMURA, Kazuto
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 10
                                                          188 GFTSVQGY-AFN-GTKLDAVYLNKNKY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NT APPLICATION DATA:
PPPLICATION NUMBER: US/07/757,342D
FILING DATE: 10-Sep-1991
CLASSIFICATION: <UNKNOWT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: DAVID G. CONLIN; DIKE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/07757342D Patent No. 6218509 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
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US-07-757-342D-5
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APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No 6806054-Endogenous, Constitutively Activated Known G
TITLE OF INVENTION: Procein-Coupled Receptors
FILE REFERENCE: AREN-207
CURRENT APPLICATION WUMBER: US/09/826,509
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION WUMBER: 60/195,747
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 1998-10-13
NUMBER: OF SEQ ID NOS: 589
SOFTWARE: Patentin Version 2.1
SEQ ID NO 587
TL---PSLIKLDLSSNLLSSFPITGLHGLTHLKLTGNHALQSLISSENFPELKVIEMPYA 476
                                                                                                                                                                                                                                                       544 SPGPFKPCEHLLDGWLIRIGVWTIAVLALTCNALVTSTVFRSPLYISPIKLLIGVIAAVN 603
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                              223 GVYSGPSL--LDVSQTSVTALPSKGLEHLKELIARNTWTLKKLPLSLSFLHLTRADLSYP
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                                                                                      477 YQCCAFG-------VCENAYKISNQWNKGDNSSMDDLHK---
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; Patent No. 6806054
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, APPLICANT: Lehmann-Bruinsma, Karin
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737 DVYELIEKSHLT 748
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; ORGANISM: Homo sapiens
US-09-826-509-587
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---LTVIYKDAFG 222
                                                                                                                APPLICANT: IGARASH1, MASAO
APPLICANT: MINGCIESH, TAKASHI
APPLICANT: MINGCIESH, TAKASHI
APPLICANT: MINGCIESH, TAKASHI
APPLICANT: MINGCIESH, TAKASHI
APPLICANT: MINGCIESH, TAZUTO
TITLE OF INVENTION: NUCLEIC ACID MOLECULARES ENCODING HUMAN LUTEINIZING
TITLE OF INVENTION: AND TRANSFORMANTS THEREOF
TILLE OF INVENTION: AND TRANSFORMANTS THEREOF
TILLE OF INVENTION: AND TRANSFORMANTS THEREOF
CURRENT APPLICATION NUMBER: US/09/461,657B
CURRENT PILING DATE: 2002-04-16
PRIOR PELLING DATE: 1991-09-10
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                                                                                          NCILNCPVAFLSFSSLINLTFISPEVIKFILLVVVPLPACLNPLLYILFNPHFKEDLVSL 834
                                                                                                                                                                            -----RKQTYVWTRSKHPSLMSINSDDVEKQSCDSTQALVTFTSSSITYDLPPSSVPS 887
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        PSTMGYMVALILLNSLCFLMMT1AYTKLYCNL----DKGDLENIWDCSMVKH1ALLLFT
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SEQ ID NO 5
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ORGANISM: Homo sapiens
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US-09-461-657B-5
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POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES

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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/741,453A
                                                                                                                                         SEE: CUSHMAN DARBY & CUSHMAN: 1615 L STREET, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT 1000MATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 919:
TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
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SEQUENCE CHARACTERISTICS:
                TITLE OF INVENTION: POLITILE OF INVENTION: ACT:
TITLE OF INVENTION: ACT:
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 NNLDEFPTAIRTLSNLKELGFHSNNIRSIPEKAFVGNPSLITIHFYDNPIQFVGRSAFQH 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:| : | : | : : : : --SIPVNAFQGLCNETLTLKLYNN 187
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                                                                                                                                                                                                                                  64 LSVFTSYLDLSMNNISQLLPNPLPSLRFLEELRLAGNALTYIPKGAFTGLYSLKVLMLQN 123
                                                                                                                 9 LLSLPVLLQL----ATGGSSPRSGVLLRGCPTHCHCEPDGRMLLRVDCSDLGLSELPSN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 SLSALQAMTLALNKIHHIPDYAFGNLSSLVVLHLHNNRIHSLGKKCFDGLHSLETLDLNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 LPELRTLTLNGASQITEFPDLTGTANLESLTLTGAQISSLP----QTVCNQLPNLQVLDL
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                                                                Gaps
                                                             Indels 312;
                                                                                                                                                     6 LLQLVLLLDLPRDLGGMGCSSP-----PCECHQEED----FRVTCKDI-
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Query Match
12.6%; Score 594; DB 3; L.
Best Local Similarity 21.9%; Pred. No. 8.3e-39;
Matches 213; Conservative 149; Mismatches 299;
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RESULT 14
US-07-741-453A-59
US-07-741-453A-59
Sequence 59, Application US/07741453A
Patent No. 6228597
GENERAL INFORMATION:
APPLICANT: LIBERT, FREDERIC
PAPLICANT: LIBERT, FREDERIC

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APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Lian
TITLE OF INVENTION: No. 6806.054-Endogenous, Constitutively Activated Known G
TITLE OF INVENTION: Protein-Coupled Receptors
FILE REFERENCE: AREN-207
CURRENT APPLICATION NUMBER: US/09/826,509
CURRENT FILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-04-07
PRIOR PRILICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: Patentin Version 2.1
LENGTH: 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31;
                 341 SKRQDTHNNAHYXVFFEEQEDELIGFGQELKNPQEETLQAFDSHYDYTICGDSEDMYCTP 400
                                                                                                     544 SPGPFKPCEHLLDGWLIRIGVWTIAVLALTCNALVTSTVFRSPLYISPIKLLIGVIAAVN 603
                                                                                                                                                                      FSVKYSAKFETKAPFSSLKVII----LLCALLALTMAAVPLLGGSKYGASPLCLPLPFGE 719
                                                                                                                                                                                                                         LSVFTSYLDLSMNNISQLLPNPLPSLRFLEELRLAGNALTYIPKGAFTGLYSLKVLMLQN 123
                                                                                                                                                                                                                                                                                                             NCILNCPVAFLSFSSLINLTFISPEVIKFILLVVVPLPACLNPLLYILFNPHFKEDLVSL 834
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                                                                                                                                                                                                                                                                                                                                                                                        693 LSKFGICKRÓAQAYRGQRVPPK---NSTDIQVÓ-------KVTHDMRQGLHNM 735
                                                                                                                    401 KSDEFNPCEDIMGYKFLRIVVWFVSLLALLGNVFVLLILLTSHYKLNVPRFLMCNLAFAD
                                                   --VQCSP
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                                                                                                                                                                                                                                                            PSTMGYMVALILLNSLCFLMMTIAYTKLYCNL----DKGDLENIWDCSMVKHIALLLFT
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---VCENAYKISNQWNKGDNSSMDDLHK-
                                                   --RDLEDFLLDF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 403, Application US/09826509 Patent No. 6806054
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ORGANISM: Homo sapiens
                                                   GMFQAQDE-
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US-09-826-509-403
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223 GVYSGPSL--LDVSQTSVTALPSKGLEHLKELIARNTWTLKKLPLSLSFLHLTRADLSYP 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 NNLDEFPTAIRTLSNLKELGFHSNNIRSIPEKAFVGNPSLITIHFYDNPIQFVGRSAFQH 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------LEITDNPYMT------SIPVNAFÖGLCNETLTLKLYNN 187
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                                                                                                           124 NOLRHVPTEALONLRSLOSLRLDANHISYVPPSCFSGLHSLRHLWLDDNALTEIPVQAFR 183
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Job time : 45 secs
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OM nucleic

Run on:

Sequence:

Word size:

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Human GPC
G protein
Human HG3
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Human G p
Human HG3
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Cancer/an
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Human LGR
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Human ova
Mouse orp
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Aaw93896
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AAW93893
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                          N-PSDB; AAX23980
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-Q=/cgn2_1/USPTO spool/US10751736/runat_12072005_084327_23907/app_query.fasta_1.2887
-Q=/cgn2_1/USPTO spool/US10751736/runat_12072005_084327_23907/app_query.fasta_1.2887
-DB=A Geneseq_16Dec04 - OFMT=fastan - SUFFIX=oligo - TRANS=human40.cdi
-LOOPEXT=0 - UNITS=bits -START=1 - END=-1 - MATRIX=oligo - TRANS=human40.cdi
-LISP=45 - DOCALIGN=200 - THR SCORE=quality - THR MIN=1 - ALIGN=15 - MODE=LOCAL
-OUTFMT=pto - NORM=ext - HRAPSIZE=500 - MINLEN=0 - MAXLEN=200000000
-NOTFMT=pto - NORM=ext - HRAPSIZE=500 - MINLEN=0 - MAXLEN=200000000
-NOTFMT=pto - NORM=ext - HRAPSIZE=500 - MINLEN=0 - MAXLEN=200000000
-NOTFMT=DTO - NORM=CT - NEG SCORES=0 - WAIT - DSPBILOCK=100 - LONGLOG
-DEV TIMEOUT=120 - WARN TIMEOUT=30 - THRRANS=1 - XGAPPEXT=60 - FGAPPOP=6
-FGAPEXT=7 - YGAPPOP=60 - YGAPEXT=60 - DELCOP=6 - DELEXT=7
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Copyright (c) 1993 - 2005 Compugen Ltd
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Result

This invention describes a novel human G-protein coupled glycoprotein hormone receptor, HG38. Glycoprotein hormone receptors are important in the endocrine system and HG38 may be involved in development and function of the skeletal muscle, spinal cord, placenta and to a lesser extent, the brain. The transgenic animal may be useful for studying tissue and temporal specific expression or activity of the HG38 receptor, as well as for studying the ability of a variety of compounds to act as modulators of HG38 receptor activity ATACCAGACTATGCCTTTGGAAACCTCTCCAGCTTGGTAGTTCTACATCTCCATAACAAT TTAAATTACAATAACCTTGATGAATTCCCCACTGCAATTAGGACACTCCCAACCTTAAA AGAATCCACTCCCTGGGAAAGAAATGCTTTGATGGGCTCCACAGCCTAGAGACTTTAGAT GCTCTGACATACATTCCCAAGGGAGCATTCACTGGCCTTTACAGTCTTAAAGTTCTTATG Arecacaccrecegerregrerecreterregrerecriecerecrecrecrecege GAGCCCGACGGCAGGATGTTGCTCAGGGTGGACTGCTCCGACCTGGGGGCTCTCGGAGCTG CTGCTCCCGAATCCCCTGCCCAGTCTCCGCTTCCTGGAGGAGTTACGTCTTGCGGGAAAC Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: (1-907)US-10-751-736-21 (1-2724) x AAW93889 907.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Query Match: DB: Sequence 907 AA Alignment Scores: Pred. No.: Score: g 셤 유 셤 8 6 8 6 음 & q Š ò ò ð ò ************ ò 셤 ઠે a 8 & **6 8 6**

LeuAsnTyrAsnAsnLeuAspGluPheProThrAlaIleArgThrLeuSerAsnLeuLys

ACAGITITICACATICCCTICTICACATITICCCCCATIAAACTGITAATIGGGGTCATCGCA CGATCCCTGAATTTGGCTTGGAACAAATTGCTATTATTCACCCCAATGCATTTTCCACT TTGCCATCCCTAATAAAGCTGGACCTATCGTCCAACCTCCTGTCGTCTTTTCCTATAACT AGCAGTATGGACGACCTTCATAAGAAAGATGCTGGAATGTTTCAGGCTCAAGATGAACGT GluLeuGlyPheHisSerAsnAsnIleArgSerIleProGluLysAlaPheValGlyAsn CCTTCTCTTATTACAATACATTTCTATGACAATCCCCATCCAATTTGTTGGGAGATCTGCT TTTCCTGATTTAACTGGAACTGCAAACCTGGAGTCTGACTTTAACTGGAGCACAGATC TCATCTCTCCTCAAACCGTCTGCAATCAGTTACCTAATCTCCAAGTGCTAGATCTGTCT TACAACCTATTAGAAGATTTACCCAGTTTTTCAGTCTGCCAAAAGCTTCAGAAATTGAC CTAAGACATAATGAAATCTACGAAATTAAAGTTGACACTTTCCAGCAGTTGCTTAGCCTC TCATCTGAAAACTTTCCAGAACTCAAGGTTATAGAAATGCCTTATGCTTACCAGTGCTGT GAACTAGGATTTCATAGCAACAATATCAGGTCGATACCTGAGAAAGCATTTGTAGGCAAC 8 8 q g 8 8 8 요 장 원 장 8 8 6 B 6 B 6 B 6 음 상 음 B & ò 셤 ò g g

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           641 GlyPheLeuSerllePheAlaSerGluSerSerValPheLeuLeuThrLeuAlaAlaLeu
                                                                               CTGAAAGTAATCATTTTGCTCTGTGCCCTGCTGGCCTTGACCATGGCCGCAGTTCCCCTG
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                                   GGTTTTTTGTCCATTTTTGCTTCAGAATCATCTTTTTCCTGCTTACTCTGGCAGCCCTG
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The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRS, AAY90643-AAY90643-Y90681), and to DNA encoding them (AAA30709-A30743) and AAA30775-A30779). The mutant proteins of the invention contain a contain a matation in a portion of the protein comprising intracellular loop 3 (CC in an disperse domain 6 (TMG). A non-endogenous amino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous proline in TMG to form a sequence X-contains of an endogenous proline in TMG to form a sequence X-contains of an endogenous proline in TMG to form a sequence X-contains of an endogenous proline in TMG to form Jus, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Pro may be endogenous, non-endogenous, or a mixture of endogenous and non-endogenous crecidues. The constitutively active GPCRs are useful for identifying antagonists and partial agonists for use as pharmaceutical containment proteins are also useful in research settings for a particular GPCR are useful for treating diseases and disorders associated with that receptors in normal and diseases and disorders associated with that receptors in normal and diseases and disorders associated with that receptors Eccause the novel mutant GPCR are constitutively active, they can be used directly for screening of compounds without the need for endogenous ligands. The present sequence corporation and human wild-type GPCR referred to in an exemplification of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
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G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug screening; agonist; antagonist.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atheroselerosis; infection; osteoathritis; allergy; osteoaporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
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                                                                                                             TGGACAAGATCAAAACACCCCAAGCTTGATGTCAATTAACTCTGATGATGTGTCGAAAAACAG
                                                                                                                            TrpThrArgSerLysHisProSerLeuMetSerlleAsnSerAspAspValGluLysGln
                                                                                                                                                                   TCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTTATGACCTG
                                                                                                                                                                                    SerCysAspSerThrGlnAlaLeuValThrPheThrSerSerIleThrTyrAspLeu
                                                      ATCTTGTTCAATCCTCACTTTAAGGAGGATCTGGTGAGCCTGAGAAAGCAAACCTACGTC
                                                                      The present invention describes antigenic peptides (I) comprising: (any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human G protein-coupled receptor GPR49 protein SEQ ID NO:422
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cc acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and 101 an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (1) can be used as GPCR modulators and in the production of specific antibody against a particular GPCR. (1) can be used as GPCR modulators and in the production of specific antibodies. The peptides for GPCRs are useful in detecting an GPCR antibodies. The peptides and antibodies are useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for disgnosing and designing the creating immune-related disease, immunological-related cell proliferative creameration-related disease, immunological-related cell proliferative diseases, or autoimmune disease, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarchritis, osteoaporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease diabetes, graft versus host cancer, cardiomyopathy, chronic and acute inflammation, allergies, crohn's disease diabetes, graft versus host cancers, parkinson's disease, multiple sclerosis, parkinson's disease, correct of disease, parkinson's disease, multiple sclerosis, pain, psoriasis, or correct of series, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, cany other disorder in which GPCRs are involved. The antibodies may be used in immunoaseays and immunodiagnosis. ABZ42523 to ABZ4269 encode correct in the correct of the correct cany other disorder in which face are involved in the correct cand in the correct canner involved in the correct canner involve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated HGPRBMY5 polypeptide. The polypeptides, polynucleotides and methods are useful for preventing, treating or ameliorating a medical condition such as a neoplastic disorder e.g. leukaemia and breast cancer; immune disorder e.g. AIDS and rheumatoid arthritis; neuronal disorder e.g. Alzheimer's disease and Parkinson's disease; respiratory disorder e.g. ovarian carcinoma and meig's syndrome; colon disease; breast disease; thalamus related disorder; amygdala related disorder; corpus callosum related disorder; caudate nucleus related disorder; hippocampus related disorder; caudate the GFCR polypeptide or its homologue. The present sequence represents the amino acid sequence of a G-protein coupled receptor used to show homology with the human G-protein coupled receptor, HGPCRBMY
                                                                                                                                                                      Parkinson's disease; respiratory disorder; bronchopulmonary disease; pancoast's syndrome; ovarian disorder; ovarian carcinoma; colon disease; Meig's syndrome; breast disease; thalamus related disorder; gene therapy; amygdala related disorder; corpus callosum related disorder; hippocampus related disorder.
                                                                                                                                             neoplastic disorder; leukaemia; breast cancer; immune disorder; AIDS; rheumatoid arthritis; neuronal disorder; Alzheimer's disease; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New G-protein coupled receptor polypeptides, designated as HGPRBMY5, useful for preventing, treating or ameliorating a medical condition related to the colon, breast, ovaries or immune system.
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Matches:
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                        ABO06467 standard; protein; 907
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16-JAN-2001; 2001US-0261781P.
19-JUL-2001; 2001US-0306605P.
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1080 TTTCCTGATTTAACTGGAACTGCAAACCTGGAGAGTCTGACTTTAACTGGAGCACAGATC 1020 840 180 909 200 300 9 220 720 780 900 960 280 PheGlnHisLeuProGluLeuArgThrLeuThrLeuAsnGlyAlaSerGlnIleThrGlu 320 161 LeuHisSerLeuArgHisLeuTrpLeuAspAspAsnAlaLeuThrGlu1leProValGln 201 IleProAspTyrAlaPheGlyAsnLeuSerSerLeuValValLeuHisLeuHisAsnAsn ArglleHisSerLeuGlyLysLysCysPheAspGlyLeuHisSerLeuGluThrLeuAsp TTAAATTACAATAACCTTGAAGAATTCCCCACTGCAATTAGGACACTCTCCAACCTTAAA GAACTAGGATTTCATAGCAACAATATCAGGTCGATACCTGAGAAAGCATTTGTAGGCAAC CCTTCTTATTACATACATTTCTATGACAATCCCATCCAATTTGTTGGGAGATCTGCT TITCAACATITACCTGAACTAAGAACACTGACTCTGAATGGTGCCTCACAAATAACTGAA GCTTTTAGAAGTTTATCGGCATTGCAAGCCATGACCTTGGCCCTGAACAAATACACAC ATACCAGACTATGCCTTTGGAAACCTCCAGCTTGGTAGTTCTACATCTCCATAACAAT AGAATCCACTCCCTGGGAAAGAAATGCTTTGATGGGCTCCACAGCCTAGAGACTTTAGAT ProSerLeulleThrIleHisPheTyrAspAsnProIleGlnPheValGlyArgSerAla TCATCTCTTCCTCAAACCGTCTGCAATCAGTTACCTAATCTCCAAGTGCTAGATCTGTCT 1021 961 321 341 셤 8 g

Conservative: Mismatches: Indels:

Gaps: (1-907)

US-10-751-736-21 (1-2724) x ABO06467

Best Local Similarity: Query Match: DB:

Percent Similarity:

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                       ACCATTGCCTACACCAAGCTCTACTGCAATTTGGACAAGGAGACCTGGAGAATATTTGG
                                                                                                                          TCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTTATGACCTG
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                                                              CCTGTGGGCTTTCTTGTCCTTCTCCTCTTTAATAAACCTTACATTATCAGTCCTGAAGTA
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                                                                                                                                                 ATCTTGTTCAATCCTCACTTTAAGGAGGATCTGGTGAGCAAAGCAAACCTACGTC
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                                                                                                                                                                                                                                                                                                                                                                                    region;
                                                                                                                                                                                                                                                                                                                                                                                 Human; G protein-coupled receptor; GPCR; transmembrane-6 intracellular-3 region; IC3; receptor.
                                                                                                                                                                                                                                                                                                                                                                    Human G protein-coupled receptor (GPCR) polypeptide
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                                                                                             TTGCCATCCCTAATAAAGCTGGACCTATCGTCCAACCTCCTGTCGTCTTTTCCTATAACT
                                                                                                    GGGTTACATGGTTTAACTCACTTAAAATTAACAGGAAATCATGCCTTACAGAGCTTGATA
                                                                                                                                   GCATTTGGAGTGTGTGAGAATGCCTATAAGATTTCTAATCAATGGAATAAAGGTGACAAC
                                                                                                                                                                                                 AlaPheGlyValCysGluAsnAlaTyrLysIleSerAsnGlnTrpAsnLysGlyAspAsn
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                                                                                                                                                                                                                                                                                                                                                                            AlavalAsnMetLeuThrGlyValSerSerAlaValLeuAlaGlyValAspAlaPheThr
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coupled receptor (GPCR) comprises substituting a specific amino acid in the transmembrane-6 region with a different amino acid, and testing for constitutive activity.

Example 1; SEQ ID NO 264; 221pp; English

The invention relates to a method for treating a non-endogenous, constitutively active version of an endogenous human G protein-coupled receptor (GPCR) that has a transmembrane-6 (TMG) region and an intracellular-3 (IC3) region, by substituting a specific amino acid in the TMG region with a different amino acid, and testing for constitutively activity. The method is useful for creating a constitutively acity extinor an endogenous human GPCR that comprises a transmembrane 6 region and an intracellular loop 3 region. The altered human GPCR cegion and an intracellular loop 3 region. The altered human GPCR colypeptides are useful for screening test compounds for identification of inverse agonists or partial agonists of GPCR polypeptides, which may have therapeutic uses. The altered GPCR may also be used in vivo or in vivo in biological research. A nucleic acid encoding the altered GPCR may be used to create a transgenic animal expressing the altered GPCR colyman G protein-coupled receptor without the need for provision of a ligand for the receptor. This is particularly useful in allowing screening of compounds against orphan receptors for which no ligand is currently known. This sequence represents a human GPCR polypeptide of the Invention.

Sequence 907 AA;

907 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 907.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: No.: Score:

(1-907)US-10-751-736-21 (1-2724) x ADC22783

È	Н	ATGGACACCTCCCGGCTCCGGTGTGCTCTGCCTGCCTGCTGCTGCTG	
qq	Н	MetAspThrSerArgLeuGlyValLeuLeuSerLeuProValLeuLeuGlnLeuAlaThr 20	
è	61	GGGGCAGCTCTCCCAGGTCTGGTGTGTT	
qq	21	GlyGlySerSerProArgSerGlyValLeuLeuArgGlyCy	
ò	121	GAGCCCGACGGCAGGATGTTGCTCAGGGTGGACTGCTCCGACCTGGGGGCTCTCGGAGCTG 180	
qa	41	GlubroAspGlyArgMetLeuLeuArgValAspCysSerAspLeuGlyLeuSerGluLeu 60	
ò	181	CCTTCCAACCTCAGGGTCTTCACCTCCTAGACCTCAGTATGAACAACATCAGTCAG	
qa	61		
à	241	CTGCTCCCCGAATCCCCTGCCCAGTCTCCGCTTCCTGGAGGAGTTACGTCTTGCGGGAAAC 300	
QQ	81		
ò	301	GCTCTGACATACATTCCCAAGGGAGCATTCACTGGCCTTTACAGTCTTAAAGTTCTTATG 360	
qq	101		
Š	361	CIGCAGAATAATCAGCTAAGACACGTACCCACAGAAGCTCTGCAGAATTTGCGAAGCCTT 420	
qq	121	LeuGlnAsnAsnGlnLeuArgHisValProThrGluAlaLeuGlnAsnLeuArgSerLeu 140	
È	421	CAATCCCTGCGTCTGGATGCTAACCACATCAGCTATGTGCCCCCCAAGCTGTTTCAGTGGC 480	
qq	141		
ò	481	CTGCATTCCCTGAGGCACCTGTGGCTGGATGACAATGCGTTAACAGAAATCCCGGTCCAG 540	
qq	161		

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ò	601	ATACCAGACTATGCCTTTGGAAACCTCTCCAGCTTGGTAGTTCTACATCTCCATAACAAT 660
a a	201	
È i	661	AGAATCCACTCCCTGGGAAAGAATGCTTTGATGGGCTCCAAGCCTAGAGACTTTAGAT 720
g	221	ArgileHisSerLeuGlyLysLysCysPheAspGlyLeuHisSerLeuGluThrLeuAsp 240
දු ද	721	
} &	781	GAACTAGGATTTCATAGCAACAATATCAGGTCGATACCTGAGAAAGCATTTGTAGGCAAC 840
: 원	261	
ò	841	CCTTCTCTTATTACAATACATTCTATGACAATCCCATCCAATTTGTTGGGAGATCTGCT 900
qq	281	ProserteuileThrileHisPheTyrAspAsnProlleGinPheValGlyArgSerAla 300
à	901	TITCAACAITIACCTGAACTAAGAACACTGACTCTGAAIGGTGCCTCACAATAACTGAA 960
අු	301	PheGlnHisLeuProGluLeuArgThrLeuThrLeuAsnGlyAlaSerGlnIleThrGlu 320
<i>&</i> 1	961	TTTCCTGATTTAACTGGAAACTGGAAAGCTGACTTTAACTGGAGCACAGATC 1020
gg	321	PheProAspLeuThrGlyThrAlaAsnLeuGluSerLeuThrLeuThrGlyAlaGlnlle 340
රු සි	1021	TCATCTCTCCTCCAAACCGTCTGCAATCAGTTACCTAATCTCCAAGTGCTAGATCTGTCT 1080
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ò	1201	CGATCGCTGAATTTGGCTTGGAACAAATTGCTATTATTCACCCCAATGCATTTTCCACT 1260
qq	401	ArgSerLeuAsnLeuAlaTrpAsnLysIleAlallelleHisProAsnAlaPheSerThr 420
ò	1261	TIGCCATCCCTAATAAAGCTGGACCTATCGTCCAACCTCCTGTCGTCTTTCCTATAACT 1320
Dp	421	LeurroSerLeullelysLeurspreuserSerksnleuleuserSerPheProlleThr 440
È	1321	GGGTTACATGGTTTAACTCACTTAAAAATTAACAGGAAATCATGCCTTACAGAGCTTGATA 1380
qq	441	GlyLeuHisGlyLeuThrHisLeuLysLeuThrGlyAsnHisAlaLeuGlnSerLeuIle 460
ò	1381	TCATCTGAAAACTTTCCAGAACTCAAGGTTATAGAAATGCCTTATGCTTACCAGTGCTGT 1440
qa	461	SerSerGluAsnPheProGluLeuLysVallleGluMetProTyrAlaTyrGlnCysCys 480
ò	1441	GCATTTGGAGTGTGTGAGAATGCCTATAAGATTTCTAATCCAATGGAATAAAGGTGACAAC 1500
qq	481	AlaPheGlyValCysGluAsnAlaTyrLysIleSerAsnGlnTrpAsnLysGlyAspAsn 500
ò	1501	AGCAGTATGGACGACCTTCATAAGAAGATGCTGGAATGTTTCAGGCTCAAGATGAACGT 1560
qa	501	SerSerWetAapAspLeuHiaLysLysAspAlaGlyMetPheGlnAlaGlnAspGluArg 520
ò	1561	GACCTTGAAGATTCCTGCTTGACTTTGAGGAAGACCTGAAAGCCCTTCATTCA
QQ	521	euGluAspPheLeuLeuAspPheGluGluAspLeuLysAlaLeuHisS

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CysSerProSerProGlyProPheLysProCysGluHisLeuLeuAspGlyTrpLeuIle
                                                             AlaValAsnMetLeuThrGljyValSerSerAlaValLeuAlaGlyValAspAlaPheThr
                                                                                                                                                                                                                                                  AspCysSerMetValLysHisIleAlaLeuLeuLeuPheThrAsnCysIleLeuAsnCys
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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, cor human polynucleotides or a polynucleotide acid sequence. Also claimed are a vector comprising the movel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a chat increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound for identifying a compound or small molecule that regulates the activity of one or more of the compound for identifying a compound or small molecule that regulates the cativity in an animal of one or more of the specification, a method for identifying a compound useful in treating compliance of or identifying a compound useful in treating compliances its activity is useful for preparing a medicament for treating compliances its activity is useful for preparing a medicament for treating compliances its activity is useful for preparing a medicament for treating compliance of a specification which is differentially expressed during pain. Note: the specification, but was obtained in electronic form directly from WIPO at the way obtained in electronic form directly from wIPO at sequence or the specification, but was obtained in electronic form directly from WIPO at
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ADES9150 standard; protein; 907
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The invention discusses a composition of the mucleic acid sequence. Also derivative or allelic variation of the mucleic acid sequence. Also claimed are a vector comprising the novel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a compound that regulates the activity of one or more of the composition, a continity in an animal of one or more of the polymetides given in the activity in an animal of one or more of the polymetides given in the compound to a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more of pain and a pharmaceutical composition comprising the one or more of pain and a pharmaceutical composition comprising the one or more of pain and a pharmaceutical composition comprising the one or more of pain and a pharmaceutical composition comprising the one or more of the special activity is useful for preparing a medicament for treating pain and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the sequence data for this patent did not form part of the printed specialication, but was obtained in electronic form directly from WIPO at the wipo.int/pub/published_pot_escored or electronic form directly from WIPO at
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(GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes a new isolated polypeptide comprising: a polypeptide or its mature form comprising a sequence not given in the specification; or a variant of (A), where one or more amino acid residues in the variant differs in no more than 15% from the amino acid sequence of the mature form. The pharmaceutical composition may be administered via oral, transdermal, rectal or parenteral route. The polypeptide, nucleic acid or antibody is useful for preparing a composition for treating or preventing a NoWX-associated disorder, e.g., cancer. This is the amino acid sequence of a transmembrane receptor homologue used in a comparison with the novel human proteins of the invention.
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 IleLeuPheAsnProHisPheLysGluAspLeuValSerLeuArgLysGlnThrTyrVal 840
                                                                                                                                                                                                                                                                                              cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical; NOVX-associated disorder; cancer; human; G protein coupled receptor 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New NOVX gene or NOVX-specific antibody, useful for preparing a composition for treating or preventing a NOVX-associated disorder, e.g.,
                                 TCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTTATGACCTG
                                                                                                       CCTCCCAGTTCCGTGCCATCACCAGCTTATCCAGTGACTGAGAGCTGCCATCTTTCCTCT
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                                                                                                                                                            ADG42628 standard; protein; 907
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(RAST/) RASTELLI L.
(SHIM/) SHIMKETS R A.
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Length: Matches: Conservative: Mismatches:

907.00 100.00% 100.00%

Percent Similarity: Best Local Similarity:

TCATCTTCCTCAAACCGTCTGCAATCAGTTACCTAATCTCCAAGTGGTAGATCTGTCT SerSerLeuProGInThrValCysAsnGlnLeuProAsnLeuGlnvalLeuAspLeuSer TACAACCTATTAGAAGATTTACCAGTTTTTCAGTCTGCCAAAGCTTCAGAAATTGAC TYASnLeuLeuGluAspLeuProSerPheSerValCysGlnLysLeuGlnLysIleAsp TTACAACATAATGAAATTTACCAAAATTAAACTTGACACTTTCCAGCAGTTGCTTAGCCTC TACAACATAATGAAATTTACAAAATTAAACTTGACACTTTCCAGCAGTTGCTTAGCCTC TACAACATAATGAAAATTAGCTTGAAAATTGACATTATTCACCCCAATGCATTTTCCACT TACAACATAATAAAAATTACACAAAATTGACAATTATCACCCCAATGCATTTTCCACT TTACCATCCCTAATAAAAATTACCCAACCTAATTATTCACCCCAATGCATTTTCCACT TTGCCATCCCTAATAAAAATTAAAAATTAAAAATTAACACCAAAAATTAAAAATTAAAAATTAAAAAA	1681 AGAATTGGAGTGTGGACCATAGCACTTACTTGTAATGCTTTGGTGACTTCA 171 ALGAGTTTTTGAATTTTTAAATTTTTTTTTTTTTTTTTT

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New constitutively active, non-endogenous version of an endogenous human G protein-coupled receptor for the identification of therapeutic compounds, such as agonists.
WPI; 2003-801247/75.
N-PSDB; ADH14255.
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Example 1; SEQ ID NO 264; 227pp; English.

The invention relates to a constitutively active, non-endogenous version of an endogenous human G protein-coupled receptor (GPCR). The GPCR is used for screening therapeutic compounds as inverse agonists, agonists or partial agonists. The GPCR can be also be used to elucidate and understand the roles of GPCRs in normal and diseased humans. The GPCR need not be purified and isolated to be used to screen for therapeutic compounds. The utility of the GPCR as a research tool is enhanced because the role of a particular receptor can be understood before the endogenous ligand is identified. The present sequence is used in the exemplification of the present invention.

Sequence 907 AA;

ignm sd. ore: rcen st L	s : 🖆 L &	<pre>cores: ilarity: Similarity: :</pre>	0 907.00 100.00% 100.00%	Length: Matches: Conservative: Mismatches:	907 907 0
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ò	н	ATGGACACC	CTCCCGGCTCGGTGT	ATGGACACCTCCCGGCTCGGTGTGCTCCTGTCCTTGCCTGTGTGTG	STGCTGCTGCTGGCGACC 60
qq	ч	MetAspTh	rSerArgLeuGlyVa		
ò	61		CTCTCCCAGGTCTGG	GGGGGCAGCTCTCCCAGGTCTGGTGTTTGCTGAGGGGCTGCCCCA	TGCCCCACACACTGTCATTGC 120
qq	21	GlyGlySe	rSerProArgSerGl	yvalleuleuArgGlyC	GlyGlySerSerProArgSerGlyValLeuLeuArgGlyCysProThrHisCysHisCys 40
à	121	GAGCCCGAC	GAGCCCGACGCAGGATGTTGCT	CAGGGTGGACTGCTCCGACCTGGGGCT	SACCTGGGGCTCTCGGAGCTG 180
QQ	41	GluProAsp	oglyArgMetLeuLe	uArgValAspCysSerA	GluProAspGlyArgMetLeuLeuArgValAspCysSerAspLeuGlyLeuSerGluLeu 60
à	181	-	CTCAGCGTCTTCAC	CTCCTACCTAGACCTC	CCTTCCAACCTCAGGGTCTTCACCTACACTAGACCTCAGTATGAACAACATCAGTCAG
Ωp	61	ProSerAsi	lllllllllllllll	rSerTyrLeuAspLeuS	ProSerAsnLeuSerValPheThrSerTyrLeuAspLeuSerMetAsnAsnIleSerGln 80
ò	241	-	SAATCCCCTGCCCAG	TCTCCGCTTCCTGGAGG	CTGCTCCCGAATCCCCTGCCCAGTCTCCGCTTCCTGGAGGAGTTACGTCTTGCGGGAAAC 300
đ	81		January Januaro Januaro	rreuArgPhereuGlud	
ò	301	GCTCTGACATACA	ATACATTCCCAAGGG	TTCCCAAGGGAGCATTCACTGGCCTTTACAGT	TACAGTCTTAAAGTTCTTATG 360
qq	101	•	rTyrlleProLysGl	yAlaPheThrGlyLeul	AlaLeuThrTyrileProLysGlyAlaPheThrGlyLeuTyrSerLeuLysValLeuMet 120
ò	361	_	TAATCAGCTAAGACA	CTGCAGAATAATCAGCTAAGACACGTACCCACAGAAGCTC	CTGCAGAATTTGCGAAGCCTT 420
QQ	121		nAsnGlnLeuArgHi	svalproThrGluAlaI	LeuGlnAsnAsnGlnLeuArgHisValProThrGluAlaLeuGlnAsnLeuArgSerLeu 140
È	421	_	GCGTCTGGATGCTAA	CCACATCAGCTATGTGC	CAATCCCTGCGTCTGGATGCTAACCACCATGTGCCCCCCAAGCTGTTTCAGTGGC 480
ф	141	-	JArgrenAspAlaAs	nHislleSerTyrVal	GINSerLeuArgLeuAspAlaAsnHisIleSerTyrValProProSerCysPheSerG1y 160
ζò	481	CIGCATICC	CCTGAGGCACCTGTGGCTGGATGACAA	GCTGGATGACAATGCG	TTAACAGAAATCCCCGTCCAG 540
đ	161		rreuArgHisteuTr	preudspaspasnalai	LeuHisSerLeuArgHisLeuTrpLeuAspAspAsnAlaLeuThrGlu1leProValGln 180

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	1 AGAATCCACTCCTGGGAAAAAAGCTTTGATGGGCTCCACAGCCTAGAGACTTTAGAT	1 TTAAATTACAATAACCTTGATGAATTCCCCACTGCAATTAGGACACTCTCCAACCTTAAA	1 GAACTAGGATTTCATAGCAACAATATCAGGTCGATACCTGAGAAAGCATTTGTAGGCAAC 	1 CCTTCTCTTATTACAATACATTTCTATGACAATCCCATCCAATTTGTTGGGAGATCTGCT 	1 TTTCAACATTTACCTGAACTAAGAACACTGACTCTGAATGGTGCCTCAAAT	1 TTTCCTGATTTAACTGGAACTGCAAGTCTGAAGTCTGACTTTAACTGCAGACAGT	1 TCATCTTCTCCAAACGTCTGCAATCAGTTACCTAATCTCCAAGTGCT 	1 TACAACCTATTAGAAGATTTACCCAGTTTTT 	CTAAGACATAATGAAATCTACGAAATTAAAGTTGAC 	CGATCGCTGAATTTGGCTTGGAACAAA 	1 TTGCCATCCCTAATAAAGCTGGACCTATCGTCCAACCTCCTGTCGTCGTTTTCCTATAACT	1 GGGTTACATGGTTTAACTCACTTAAAATTAACAGGAAATCATGCCTTACAGAGCTTGATA	1 TCATCTGAA 	1 GCATTTGGAGTGTGTGAGAATGCCTATAAGATTTCTAATCAATGGAATAAAGGTGACAAC 	AGCAGTATGGACCTTCATAAGAA	GACCTTGAAGATTTCCTGCTTGA 	1 TGTTCACCTTCCCCAGGCCCCTTCAAACCTGTGA	4 —
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                                                                AGCACCATGGGCTACATGGTCGCTCTCATCTTGCTCAATTCCCTTTGCTTCCTCATGATG
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                                                                                                                             661 GluArgGlyPheSerValLysTyrSerAlaLysPheGluThrLysAlaProPheSerSer
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                                       GlyPheLeuSerIlePheAlaSerGluSerSerValPheLeuLeuThrLeuAlaAlaLeu
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ADN40013 standard; protein; 907 AA

ADN40013 ID ADN4

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The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
other diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
of determining the presence or absence of a pathological cell in a
of determining the presence or absence of a pathological cell in a
of determining the presence or absence of a pathological cell in a
of determining the presence or absence of a pathological cell in a
of the invention or by detecting a polypeptide of the invention. The
invention also relates to expression vectors and host cells comprising a
concleic acid of the invention, antibodies which specifically bind a
polypeptide of the invention, use of such antibodies for drug targeting;
and methods of screening for modulacors of activity or expression of the
polypeptides and nucleic acids. The nucleic acids, polypeptides,
cancer and other conditions such as sporiasis, ischaemia, heart disease,
atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
everyacularisterian syndromes, scarring and uterine fibroids. They may
close be useful in wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                     Human, differential expression, cancer, angiogenic disorder,
fibrotic disorder, psoriasis, ischaemia, heart disease, atherosclerosis,
inflammatory disease, autoimmune disease;
                                                                                                                                                                                    retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine.
Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C383
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E, Zlotnik A;
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Murray R, Watson SR,
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20-FEB-2002; 2002US-0359077P.
29-MAR-2002; 2002US-0368809P.
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29-NOV-2001; 2001US-0334393P.
03-DEC-2001; 2001US-035394P.
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08-JAN-2002; 2002US-0347211P.
10-JAN-2002; 2002US-0347349P.
08-FEB-2002; 2002US-0355250P.
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22-JUL-2002; 2002US-0397845P.
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16-JUL-2002; 2002US-0396839P.
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N-PSDB; ADN39796.
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### Sequence 907 AA; Alignment Scores: 0	Qy 721 TTAAATTACAATAACCTTGAATTACCCCACTGCAATTAGGACACTCTCCCAACCTTAAA 780 Db 241 LeuAsnTyrAsnAsnAsnLeuAspGluPheProThrAlaileArgThrLeuSerAsnLeuLys 260 Qy 781 GAACTACGATTCCATAGCAACAATATCAGGTCCATACCTGAGAAAGCATTTGTAGGCAAC 840 Db 261 GluLeuGlyPheHisSerAsnAsnIleArgSerIleProGluLysAlaPheValGlyAsn 280 Qy 841 CCTTCTCTTATTACAATACATTCTATGACAATCCCATCCAATTGTTGGGAGATCTGCT 900 CD

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13-NOV-2001; 2001US-0350666P.
21-NOV-2001; 2001US-0332464P.
29-NOV-2001; 2001US-03323464P.
03-DBC-2001; 2001US-0335394P.
14-DEC-2001; 2001US-0340376P.
08-JAN-2002; 2002US-0347349P.
08-FBB-2002; 2002US-0355250P.
13-FBB-2002; 2002US-0355250P.
29-MAR-2002; 2002US-0356714P.
29-MAR-2002; 2002US-0356907P.
04-APR-2002; 2002US-036809P.
04-APR-2002; 2002US-0372246P.
                     13-NOV-2002; 2002WO-US036810
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Mack DH,
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                                       CTGGGTGGCAGCAAGTATGGCGCCTCCCCTCTGCCTTTGCCTTTTGGGGAGCCC
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The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
other diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
content by detecting a nucleic acid at least 80% identical to those of
the invention also relates to expression vectors and host cells comprising a
invention also relates to expression vectors and host cells comprising a
concleic acid of the invention; antibodies which specifically bind a
polypeptide of the invention; antibodies for drug targeting;
and methods of screening for modulators of activity or expression of the
polypeptides and nucleic acids. The nucleic acids, polypeptides,
and methods are useful for diagnosing, prognosing and treating
cancer and other conditions such as psoriasis, ischaemia, heart disease,
therosclerosis, inflammatory diseases, autoimmune diseases, retinal
neovascularistation syndromes, acarring and uterine fibroids. They may
also be useful in wound healing and in contraception. The present
sequence represents a polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGGGCAGCTCTCCCAGGTCTGCTGCTGAGGGGCTGCCCCACACACTGTCATTGC 120
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Murray R, Watson SR, Wilson KE, Zlotnik A;
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05-JUN-2002; 2002US-0386614P.
16-JUL-2002; 2002US-0396839P.
22-JUL-2002; 2002US-0397775P.
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09-SEP-2002; 2002US-0409450P.
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21	GlyGlySerSerProArgSerGlyValLeuLeuArgGlyCysProThrHisCysHisCys 40	Š	1201
121	GAGCCCGACGCAGGATGTTGCTCAGGGTGGACTGCTCCACCTGGGGGCTCTCGGAGCTG 180	අු	401
Į .	GLURIOABDGLYAIGHELDEUDAGGAGATABDCYSSEIABDGCGIYDEUGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	à	1261
181	CCTTCCAACCTCAACGTCTCACCTCCTACCTAAACCTCAACTACAACTACAGTCAS 240	අු	421
241		දු දු	1321
81	LeuLeuProAsnProLeuProSerLeuArgPheLeuGluGluLeuArgLeuAlaGlyAsn	ò	1381
301	GCTCTGACATACCTATCCCAAGGGAGCATTCACTGGCCTTTACAGTCTTAAACTTCTTATG 360	q	461
101	Ataneuinriyrilekrobys61yAtarneinroLyneuiyrserneungsvalheumet	ð	1441
361	CTGCAGAATAATCAGCTAAGACA.CGTACCCACAGAAGCTCTGCAGAATTTGCGAAGCCTT Leuginka agama	q	481
421	CAATCCCTGCGTCTGGATGCTAACCACATCAGCTATGTGCCCCCCAAGCTGTTTCAGTGGC	ò	1501
141		අ	501
481	CTGCATTCCCTGAGGGACCTGTGGCTGGATGACATGAGTTAACAGAAATCCCCGTCCAG	∂ 8	1561
161	LeuHisSerLeuArgHisLeuTrpLeuAspAspAsnAlaLeuThrGluIleProValGln	ò	1621
541	GCTTTTRGAAGTTTATCGGCATTGCAAGCCATGACCTTGGCCCTGAACAAATRCACCAC 6	đ	541
181	AlaPheArgSerLeuSerAlaLeuGlnAlaMetThrLeuAlaLeuAsnLysILeH1sH18 2	à	1681
601	ATACCACACTATGCCTTTGGAAACTTCTCCAGCTTGGTAGTTCTACATCTCATAACAAT 660 	qa	561
661	AGAATCCACCTGGGAAAGAAATGCTTTGATGGGCTCCACAGGCTTAGAGACTTTAGAT	Š	1741
221		<u>a</u> è	581
721	TTAAATTACAATAACCTTGATGAATTCCCCACTGCAATTAGGACACTCTCCAACCTTAAA 7	7 6	601
241	LeuAsnTyrAsnAsnLeuAspGluPheProThrAlaIleArgThrLeuSerAsnLeuLys 2	à	186
781	GAACTAGGATTTCATAGCAACAATATCAGGTCGATACCTGAGAAAGCATTTGTAGGCAAC 84	Ωp	62
261	GluLeuGlyPheHisSerAsnAsnileArgSerileFroGluLySAlarheValulyAshi	È	192
841	CCITCTCTTATACAATACATTTCTATGACAATCCCATCTGATTGAT	Ωp	64.
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301	11 LAMCA1 INCLIGANCIAMONICACION CONTROLLO CONT	qa	661
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100	111CC164111Anc1664hc16C4haCC1664hc461C164hC164hc166hc46hc1	qq	681
321	Pherroaspleuinrolyinralaasnueudluserleuinrueunturalaadinie 340	ò	2101
021	TCATCITCTTCCTCAAACCGTCIGCAATCAGTTACCTAATCTCCAAGTGCTAGATCTGTCT 1080	qu	701
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180	TACAACCTATTAGAAGATTTACCCAGTTTTCAGTCTGCCAAAAACTTCAGAAAATTTGACTTTAGATTAGAAAAATTTGACTTAGAAAAAATTTGACTAGAAAAAAAA	ηD	721
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141 381	CTAGGACATAGTGACATCTAGGAATTGAGGTGACATTTCAGCACTTGCTTG	q	741

1201	CGATCGCTGAATTTGGCTTGGAACAAATTGCTATTATTCACCCCAATGCATTTTCCACT	1260 420
1261	CATCCCTAATAAAGCTGGACCTATCGTCCAACCTCCTGTC 	1320 440
1321	GTTACAT	1380 460
1381	ATCTGA SerGlu	4 8
	GCATTTGGAGTGTGTGAGAATGCCTATAAGATTTCTAATCAATGGAATAAAGGTGACAAC 	1500 500
	AGTATO	1560 520
1561	GACCTTGA AspleuGl	1620 540
1621	TTCACCTTCCCCAGGCCCCTTCAAACCCTGTGAACACCTGCTT 	1680 560
1681	MTTGGAGTGTGGACCATAGCAGTTCTGGCACTTACTTGTAATGCTTTGGTGACTT 	1740 580
1741	ACAGITITCAGATCCCCTCTGTACATITCCCCCATIAAACTGTTAATTGGGGTCATCGCA 	1800 600
1801	GCAGTGAACATGCTCACGGAGTCTCCAGTGCCGTGCTGGCTG	1860 620
1861	TITGGCAGCITIGCACGACAIGGIGCCTGGIGGAGAANGGGGITGGTTGCCATGICATT	92
1921	GGTTTTTTGTCCATTTTTGCTTCAAATCATCTGTTTTCCTGCTTACTCTGGCAGCCCTG	98
1981	IGGGTTCTCTGTGAAATATT 	2040 680
2041	CTGAAAGTAATGATTTTGCTCTGTGCCCTGCTGGCCTTGACCATGGCC 	2100
2101	CTGGGTGGCAGCAAGTATGGCGCTCCCCTCTCTGCCTGTTTGCCTTT 	2160 720
2161	AGCACCATGGGCTACATG	2220 740
2221	ACCATTGCCTA	2280 760

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22-JUL-2002; 2002US-0397775P.
22-JUL-2002; 2002US-0397845P.
09-SEP-2002; 2002US-0409450P.
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                                                                                                                                 ATTAAGTITTATCCTTCTGGTAGTCCCACTTCCTGCATGTCTCAATCCCCTTCTTAC
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2001US-0334393P.
2001US-0334394P.
2001US-0335394P.
2002US-034731IP.
2002US-034731IP.
2002US-0352550P.
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29-NOV-2001;
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16-JUL-2002;
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The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
other diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
content by detecting a nucleic acid at least 80% identical to those of
the invention or by detecting a polypeptide of the invention. The
convention also relates to expression vectors and host cells comprising a
convention also relates to expression vectors and host cells comprising a
concleic acid of the invention; antibodies which specifically bind a
concleic acid of the invention; use of such antibodies for drug targeting;
and methods of screening for modulators of activity or expression of the
colypeptides and nucleic acids. The nucleic acids, polypeptides,
antibodies and methods are useful for diagnosing, prognosing and treating
cancer and other conditions such as psoriasis, ischaemia, heart disease,
atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
neovascularistaion syndromes, scarring and uterine fibroids. They may
also be useful in wound healing and in contraception. The present
                                                                                                                                                                                                                                  ce of a pathological cell in a patient, or treating cancer, comprises detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300
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Wilson KE, Zlotnik A;
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                                                                                                                                                                                                                            Determining the presence or absence of
                                                                                                                                                                                                                                                              useful for diagnosing, prognosing or ta
a nucleic acid in a biological sample.
                                                       nsburg WM,
Watson SR,
(EOSB-) EOS BIOTECHNOLOGY INC.
                                                       Ginsburg
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Murray R,
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Transgenic mouse; neurological disorder; adrenal gland disorder;

transgenic mouse; neurological disorder; adrenal gland disorder;

colon disorder; intestinal disorder; cardiovascular disorder;

w colon disorder; blood disorder; immune disorder; bone disorder;

joint disorder; metabolic disorder; immune disorder; cancer;

kidney disorder; metabolic disorder; nutritive disorder; cancer;

w kidney disorder; uterus disorder; prostate disorder; testis disorder;

skin disorder; stomach disorder; pancreas disorder; spleen disorder;

thymus disorder; thyroid disorder; matiparkinsonian; antimanic;

trycetatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;

CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;

virucide; hepatocropic; antibarcerial; antianaemic; antidiabetic;

virucide; hepatocropic; antibarcerial; antianaemic; antidiabetic;

immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
                                                            2700
                                                                                The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
SerCygAspSerThrGlnAlaLeuValThrPheThrSerSerSerIleThrTyrAspLeu
                                                            CCTCCCAGTTCCGTGCCATCACCAGCTTATCCAGTGACTGAGAGCTGCCATCTTTCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina
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Zeng H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3A, Bergmann JE, Gragerov A, Hohmann J,
Mcilwain KL, Pavlova MN, Vassilatis D,
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                                                                                                                                                           ADO29408 standard; protein; 907
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cc from the trasngenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising cromber by probles wiltch hybridise to GPCR polymorleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may diseased in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, disease, depression, diabetic neuropathy, Parkinson's disease or schizophrenia); disorders of the adrenal gland; disorders of the colon or intestine (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel cyndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders; blood disorders (e.g., anomania or leuksemia); immune disorders (e.g., autoimmune disorders or AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid arrhitals, gout or osteoporosis); metabolic or nutritive disorders or cobesity, enzyme deficiency-related diseases or vitamin deficiency-related diseases); and disorders of the kidney, liver, lung, breast, ovary, cuterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thymus and thymus and chyroid (e.g., cancers). The present sequence represents a GPCR of the invention. Note: The full sequence data for this patent did not form part cof the printed specification; those sequences not shown were obtained in electronic format directly from WIPO at
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                                                                                                    cytostatic; epidermal growth factor receptor modulator; identification; therapeutic response; cancer; EGFR; biomarker.
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                                                                                protein-coupled receptor 49 protein.
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                   ADQ80369 standard; protein; 907
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N-PSDB; ADQ80249.
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Best Local Similarity:
                                                                                                                                                        WO2004063709-A2
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This sequence represents the human G protein-coupled receptor (GPCR) known as HG38. The HG38 protein and corresponding nucleic acid, may be used in the method of the invention for detecting colon or lung cancer. The first method involves performing an assay to determine the amount of HG38 in a sample of colon or lung tissue, and comparing the amount of protein to standard, thus detecting expression of protein in sample, where differential expression of protein in sample,
                                                                                                                                                                                                                                801 IleLysPheIleLeuLeuValValValProLeuProAlaCysLeuAsnProLeuLeuTyr
                                                                                                                                                     TGGACAAGATCAAAACACCCCAAGCTTGATGTCAATTAACTCTGATGATGTCGAAAAAAGAG
                                                                                                                                                                841 TrpThrArgSerLysHisProSerLeuMetSerlleAsnSerAspAspValGluLysGln
                                                                                                                                                                                           TCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTTATGACCTG
                                           ATTAAGTTTATCCTTCTGGTGGTAGTCCCACTTCCTGCATGTCTCAATCCCCTTCTCTAC
                                                                                                              ATCTTGTTCAATCCTCACTTTAAGGAGGATCTGGTGAGCCTGAGAAAGCAAACCTACGTC
                                                                                                                        human; G protein-coupled receptor; GPCR; HG38; colon; lung; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting colon or lung cancer, by determining amount of protein sample, comparing amount of protein to standard, and differential expression of protein in sample indicates colon or lung cancer.
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                                                      AGCAGTATGGACGACCTTCATAAGAAGATGCTGGAATGTTTCAGGCTCAAGATGAACGT
                                                                                                                                                                                                                  CysSerProSerProGlyProPheLysProCysGluHisLeuLeuAspGlyTrpLeuIle
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               TIGCCATCCCTAATAAAGCIGGACCTAICGICCAACCICCIGICGICTITICCIATAACT
                                                                                   GGGTTACATGGTTTAACTCACTTAAAATTAACAGGAAATCATGCCTTACAGAGCTTGATA
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standard is diagnostic of colon or lung cancer. The second method involves hybridizing a composition comprising the HG38 coding sequence, or its complement, and a labelling moiety, to nucleic acids of a sample colon or lung tissue under conditions to form at least one hybridization complex, detecting hybridization complex formation, and differential expression of the polynuclectide in the sample relative to the standard and is diagnostic of a colon or lung cancer. This first method enables earlier diagnostic of a colon or lung cancer. This first HG38 antibodies are useful for treating colon or lung cancer.	ment Scores: No.: 907 No.: 907.00 Matches: 907 Sint Similarity: 100.00\$ Mismatches: 0 Match: 100.00\$ Mismatches: 0 Gaps: 0	-736-21 (1-2724) x ADR67868 (1-907) 1 ATGGACACCTCCCGGCTCGGTGCTCCTGTCCTTGCCTGTGCTGCTGC	MetAspThrSerArgLeuGlyValLeuLeuSerLeuProValLeuLeuGlnLeuAlaThr GGGGGCAGCTCTCCCAGGTCTGGTGTTGCTGAGGGGTGCCCCACACACTGTCATTGC	21 GIYGIYSETSETPIOATGSETGIYVALLEULEUARGGIYCYBPFOINTHIBCYSHIBCYS 40 121 GAGCCCGACGGCAGGATGTTGCTCAGGGTGGACTGCTCCGACCTGGGGCTCTCGGAGCTG 180	41 GlubroAspGlyArgMetLeuLeuArgValAspCysSerAspLeuGlyLeuSerGluLeu 60	181 CCTTCCAACCTCAGCGTCTTCACCTCCTACACCTCAGTATGAACAACATCAGTCAG	241 CTGCTCCCGAATCCCCTGCCCAGTCTCCGCTTCCTGGAGAGATTACGTCTTGCGGAAAC 300	301 GCTCTGACATACATTCCCAAGGGAGCATTCACTGGCCTTTACAGTCTTAAAGTTCTTATG 360 	CTGCAGAATAATCAGCTAAGAAGTACCCACAGAGTCTGCAGAATTTTGCGAAGCCTT		421 CAATCCCTGCGTCTGGATGCTAACCACATCAGCTATGTGCCCCCAAGCTGTTTCAGTGGC 480	481 CTGCATTCCCTGAGGCACCTGTGGCTGGATGACAATGCGTTAACAGAAATCCCCGTCCAG 540 	541 GCTTTTAGAAGTTTATCGGCAFTGCCACCACACACCCTGGCCTGG		601 ATACCAGACTATGCCTTTGGAAACCTCTCCAGCTTGGTAGTTCTACATCTCCATAACAAT 660	201 ileProAspTyrAlaPheGlyAsnLeuSerSerLeuValValLeuHisLeuHisAsnAsn 220	661 AGAATCCACTCCCTGGGAAAGAAATGCTTTGATGGGCTCCACAGCCTAGAGACTTTAGAT 720	721 TTAARTTACAATAACCTTGATGAATTCCCCACTGCAATTAGGACACTCTCCAACCTTAAA 780
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Sequence 264, Application US/09170496D

Pacent No. 6555339
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein TITLE OF INVENTION: No. 6555339-Endogenous, CORREST APPLICANTON NUMBER: US/09/170,496D
CURRENT APPLICANTON NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ 1D NOS: 294
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US-09-252-991A-2839

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-0=/CQ2_2_1/USPTO_spool/USS10751736/runat_12072005_084329_23946/app_query.fasta_1.2887
-DS=ISBUGG PAtentes AA -QFMT=fastan -SUFFIX=01i.rai -MINNATCH=0.1 -LOOPCIC=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=01igo -TRANS=human40.cdi
-USPAT=pto -UNITS=bits -START=1 -END=-1 -MATRIX=01igo -TRANS=human40.cdi
-USFRT=pto -UNITS=bits -START=1 -END=-1 -MATRIX=01igo -TRANS=human40.cdi
-USFRT=pto -NORM=ext -HEAFGIZE=500 -MINIEN=0 -MAXIEN=200000000
-USER=US10751736_@CGN 1 1_53 @runat_12072005_084329_23946 -NCPU=6 -ICPU=3
-NO WMAP -LARREGQUERY -NEG SCORRS=0 -WAIT -DSPBELOKE-100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THRRANS=1 -XGAPDF=60 -XGAPEXT=60 -FGAPOP=6
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                                                                      SerThrMetGlyTyrMetValAlaLeuIleLeuLeuAenSerLeuCysPheLeuMetMet
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                    GGGTTACATGGTTTAACTCACTTAAAATTAACAGGAAATCATGCCTTACAGAGCTTGATA
                                            TCATCTGAAAACTTTCCAGAACTCAAGGTTATAGAAATGCCTTATGCTTACCAGTGCTGT
                                                                                        GCATTTGGAGTGTGTGAGAATGCCTATAAGATTTCTAATCAATGGAATAAAGGTGACAAC
                                                                                                AlaPheGlyValCysGluAsnAlaTyrLysIleSerAsnGlnTrpAsnLysGlyAspAsn
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Sequence 17184, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J Rubenfield et al.
APPLICANT: Marc J Rubenfield et al.
APPLICANT: Marc J Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENDE: 107196, 136
CURRENT APPLICATION NUMBER: US 60/074, 788
PRIOR APPLICATION NUMBER: US 60/094, 190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

LENGTH: 131
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Gaps:
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US-09-252-991A-18526
; Sequence 18526, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AM
; TITLE OF INVENTION: AERUGINOSA FOR DIAGE
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Pred. No.:
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Percent Similarity: 1
Query Match:
DB:
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US-09-252-991A-17184
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US-09-252-991A-17184
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Sequence 2, Application US/09153593A

Sequence 2, Application US/09153593A

PERENT NO. 6174994

APPLICANT: ELSHOURBAGY, NABIL A

APPLICANT: LI, XIAPOTONG

APPLICANT: BESENCENA, DERK J

TITLE OF INVENTION: NOVEL 7TM RECEPTOR (H2CAA71)

FILE REPERENCE: GH-70055-1

CURRENT PILING DATE: 1998-09-15

EARLIER APPLICATION NUMBER: 08/866,757

EARLIER PILING DATE: 1997-05-30

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FASTSEQ for Windows Version 3.0
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ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-TELECOMMUNICATION INFORMATION:
TELERHONE: 610-407-0701
TELEFAX: 610-407-0701
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
CORRESPONDENCE ADDRESS:
                                                                                 ADDRESSEE: RATNER & 1
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Best Local Similarity:
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LENGTH: 644
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APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. RUBENFIELD AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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APPLICANT: BERGSMA, DERK J
TITLE OF INVENTION: NOVEL 7TM RECEPTOR (H2CAA71)
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Matches:
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Matches:
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                                                    PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILLING DATE: 1999-02-18
PRIOR FILLING DATE: 1998-02-18
PRIOR PILLING DATE: 1998-02-18
PRIOR PILLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18526
LENGTH: 135
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PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 17449

LENGTH: 268
                   FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
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Sequence 17449, Application US/09252991A
Patent No. 6551795
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GENERAL INFORMATION:
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US-09-252-991A-25344

US-09-252-991A-25344

Sequence 25344, Application US/09252991A

Sequence 25344, Application US/09252991A

Retent No. 6551795

GENERAL INFORMATION:

TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: UNMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR PELING DATE: 1998-02-18

PRIOR PELING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 25544

LENGTH: 118

LENGTH: 118
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PAPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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Mismatches:
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Matches:
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EARLIER APPLICATION NUMBER: 60/092,956
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 258
LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 AlaAlaAlaAlaGlyAspArgGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 GCTGCTGCAGCTGGCGACCGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25344
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0.88%
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                                                                                                                      TYPE: PRT
CRGANISM: Homo sapiens
US-09-482-273-258
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Best Local Similarity:
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Best Local Similarity:
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US-09-252-991A-24978
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Pred. No.:
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Sequence 809, Application US/10101464A

Patent No. 668041

APPLICANT: Strabala, Timothy

APPLICANT: Nievembnizen, Nicolaas

APPLICANT: Nievembnizen, Nicolaas

APPLICANT: Higgins, Colleen M.

TITLE OF INVENTION: and Timit Use in the Modification of Plant Cells

TITLE OF INVENTION: and Timit Use in the Modification of Plant Cell Signaling

FILE REFERENCE: 11000.1020c2

CURRENT APPLICATION NUMBER: US/10/101,464A

FURENT APPLICATION NUMBER: 09/704,302

PRIOR PELING DATE: 2000-11-01

PRIOR PELING DATE: 1999-01-12

PRIOR APPLICATION NUMBER: 60/162,866

PRIOR PELICATION NUMBER: 60/162,866

PRIOR PELICATION NUMBER: 1999-01-12

PRIOR APPLICATION NUMBER: 60/162,866

PRIOR PELING DATE: 1999-01-12

PRIOR PELING DATE: 1999-01-12

PRIOR APPLICATION NUMBER: 2000-01-11

NUMBER OF SEQ ID NOS: 989

SEQ ID NO 809

LENGTH: 1133
                          US-10-751-736-21 (1-2724) x US-10-101-464A-809 (1-1133)
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Matches:
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Mismatches:
Indels:
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Sequence 258, Application US/0948273
Sequence 258, Application US/0948273
Sequence 258, Application US/0948273
SETILE REPRENCE: POSJ091
STILE REPRENCE: POSJ091
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
SARLIER FILING DATE: 1999-07-14
EARLIER FILING DATE: 1998-07-15
SARLIER APPLICATION NUMBER: 60/092,921
SARLIER APPLICATION NUMBER: 60/092,921
SARLIER APPLICATION NUMBER: 60/092,921
SARLIER APPLICATION NUMBER: 60/092,922
                                                                                                                                                                 US-10-751-736-21 (1-2724) x US-09-153-593-2 (1-644)
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Matches:
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Pred. No.:
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            Alignment Scores:
Pred. No.:
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RESULT 14
US-09-270-767-60345
; Sequence 60345, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: NUMBLE: 0326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT PILING DATE: 1999-03-17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 60345
: LENGTH: 203
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Conservative:
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Mismatches:
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APPLICANT: ROSEN et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: PZ030P1
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT PILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
RARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,922
EARLIER APPLICATION NUMBER: 60/092,926
EARLIER APPLICATION NUMBER: 60/092,956
                                                                                                                                                                                Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                   56 CGACCGGGGGCAGCTCTCCCAGGT
                                                                                   ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28201
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  PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
SEQ ID NO 28201
LENGTH: 161
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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Sequence 28441, Application US/09252991A

Sequence 28441, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT PELING DATE: 1999-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PLING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 28441

LENGTH: 157
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Patent No. 6551795
GENERAL INFORMATION: WILLIAM OF APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS; TITLE OF INVENTION: AERGIGINGSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERGIGINGSA FOR DIAGNOSTICS AND THERAPEUTICS
TILLE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
                                                                                                                                                                                                                                                                                                                                              US-10-751-736-21 (1-2724) x US-09-252-991A-24978 (1-149)
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Matches:
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Matches:
Conservative:
Mismatches:
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PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 24978 LENGTH: 149
                                                                                                                                                                                                                                                                                                                                                                                                                         36 ThrArgProGlyArgAlaAlaPro 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                 TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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US-09-252-991A-28201
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; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 167
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-482-273-167
Alignment Scores: 91.2 Length: 207
Score: 8.00 Matches: 8
Fercent Similarity: 100.00$ Mismatches: 0
Best Local Similarity: 100.00$ Mismatches: 0
Query Match: 4 Gaps: 0
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Search completed: July 13, 2005, 04:00:05 Job time: 75 secs

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Title: Perfect score:

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Sequence 16, Application US/09965536A

PUBLICATION NO. USZ000027323A1

GENERAL INFORMATION:
APPLICANT: FEDER, J. N.
APPLICANT: RAMANATHAN, C. S.
APPLICANT: RAMANATHAN, C. S.
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMYS, TITLE OF INVENTION: BYPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES
FILE REPERENCE: DOOALNP
CURRENT FILING DATE: 2001-09-26
PRIOR PILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                               484, App
1330, Ap
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                                                      US-09-965-536A-16
US-009-970-944-26
US-10-255-264-422
US-10-255-027-849
US-10-295-027-946
US-10-295-027-1331
US-10-295-027-1330
US-10-295-027-1330
US-10-295-027-1330
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US-10-295-027-1330
US-10-205-027-1330
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US-10-205-027-1330
US-10-205-027-1330
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US-10-205-027-1336-6
US-10-207-336-6
                    DB
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No.
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-MODEL=frame+ n2p.model - DEV=xlh
-MODEL=frame+ n2p.model - DEV=xlh
-O=/CgnZ 1/USPTO gpool/USI0751736/runat_12072005_084330_23973/app_query.fasta_1.2887
-D=Fublished Applications AA -QFWT=fastan -SUFFIX=oli.rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 - RND=-1 -MATRIX=oligo
-INSTATE - DECALLIGN=200 -THR SCORE=quality - THR MIN=1
-ALIGN=15 - MODE=LOCAL -OUTFWT=pto -NORM=ext - HEAPSIXE=500 -MINLEN=0
-MAXLEN=200000000 -USER=USI0751736 @CGN 1 1 278 @runat 12072005 084330_23973
-NCPU=5 - ICPU=3 -NO MMAP -LARGEQUERY NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMBOÜT=120 -WARN TIMBOUT=30 -THRRADS=1 -XGAPOP=60 -XGAPEXT=60
                                                                                                             July 13, 2005, 03:40:32 ; Search time 194.5 Seconds (without alignments) 10821.262 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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| cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                           - protein search, using frame_plus_n2p model
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; PRIOR APPLICATION NUMBER: 60/310,436
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 16
; LENGTH: 907
; TYPE: PRT
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	Oy 2161 AGCACCATGGGCTACATGGTCGCTCTCATCTTGCTCATTGCTTCCTCATGATG 2220	Qy 2221 ACCATTGCCTACACCAAGCTCTACTGCAATTTGGACAAGGGAGACCTGGAGAATATTTGG 2280 Db 741 ThrileAlaTyrThriysLeuTyrCysAsnLeuAspLysGlyAspLeuGluAsnIleTrp 760	Qy 2281 GACTGCTCTATGGTAAACACATTGCCCTGTTGCTCTTCACCAACTGCTCTAAACTGC 2340 Db 761 AspCysSerMetValLysHisIleAlaLeuLeuLeuLeuPheThrAsnCysIleLeuAsnCys 780	Oy 2341 CCTGTGGCTTTCTTGTCCTCTTTTAATAACCTTACAGTCTGAAGTA 2400	OY 2401 ATTAAGTTTATCCTTCTGGTGGTAGTCCCACTTCCTGCATGTCTCAATCCCCTTCTCTAC 2460	Qy 2461 ATCTIGITCAATCCTCACTITAAGGAGGATCTGGTGAGCCTGAGAAACCAAACC	Oy 2521 TGGACAAGATCAAAACACCCCAAGCTTGATGTCAATTAACTCTGATGATGTCGAAAAACAG 2580 Db 841 TTpThrArgSerLysHisProSerLeumetSerlleasnSerAspAspValGluLysGln 860	Oy 2581 TCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTTATGACCTG 2640	Oy 2641 CCTCCCAGTTCCGTGCCATCACCAGCTTATCCAGTGACTGAGAGCTGCCATCTTTCCTCT 2700	Oy 2701 GTGGCATTTGTCCCATGTCTC 2721	RESULT 4 US-10-225-567A-422 Sequence 422, Application US/10225567A Sequence 422, Application US/10225567A Sequence 422, Application US. US2030113798A1 GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Burmer, Glena C. APPLICANT: Burmer, Glena C. APPLICANT: Rough, Christine L. TITLE OF INVENTION: ANTIGENIC FEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS FILE REFERENCE: 1920-4-4 CURRENT FILING DATE: 2001-12-19 PRIOR PILING DATE: 2001-12-19 PRIOR PELING DATE: 2001-12-19 PRIOR PELING DATE: 2001-12-19 NUMBER OF SEQ ID NOS: 2292 SOFTWARE: PALENTIN version 3.1

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; ORGANISM: Homo sapiens
US-10-295-027-849
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APPLICANT: AZIZ, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Marck, David H.
APPLICANT: Marck, David H.
APPLICANT: March, Substance, Substance, Steeling for Modulators of Cancer, CHERRY APPLICANT: Wethods of Screening for Modulators of Cancer, TITLE OF INVENTION: Methods of Screening for Modulators of Cancer, TITLE OF INVENTION: Methods of Screening for Modulators of Cancer, TITLE OF INVENTION: Methods of Screening for Modulators of Cancer, TITLE OF INVENTION: Methods of Screening for Modulators of Cancer, TITLE OF INVENTION: Methods of Screening for Modulators of Cancer, FILING DATE: 2000-11-13
FRICK REPLICATION NUMBER: US 60/350, 333
FRICK FILING DATE: 2001-11-13
FRICK APPLICATION NUMBER: US 60/332, 464
FRICK APPLICATION NUMBER: US 60/334, 393
FRICK RILING DATE: 2001-11-29
FRICK RILING DATE: 2001-11-29
FRICK RILING DATE: 2001-12-14
FRICK RILING DATE: 2002-01-10
FRICK RILING DATE: 2002-02-13
FRICK REPLICATION NUMBER: US 60/347, 319
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US-10-295-027-946
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Sequence 946, Application US/10295027
Publication No. US20030232350A1
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                    2341 CCTGTGGCCTTTCTTGTCCTTCTCCTCTTTAATAACCTTACATTTATCAGTCCTGAAGTA
781 ProValAlaPheLeuSerPheSerSerLeuIleAsnLeuThrPheIleSerProGluVal
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; TYPE: PRT ; ORGANISM: Homo Bapiens US-10-295-027-1331	Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Best Local Similarity: 100.00\$ Mismatches: Mismatch	100.00* Indels: 15 Gaps:	US-10-751-736-21 (1-2724) X US-10-295-027-1331 (1-907) Qy 1 ATGGACACCTCCCGGCTCTCGTGTTGCTTGTCTTGCTTGTTGCTGTTGCTGC	Db 1 MetAspThrSerArgLeuGlyValLeuLeuSerLeuProValLeuLeuGlnLeuAlaThr 20 Qy 61 GGGGGAGCTCTCCCAGGTCTTGCTGAGGGGCTGCCCCACATTGC 120	Db 21 GlyGlySerSerProArgSerGlyValLeuLeuArgGlyCysProThrHisCysHisCys 40 Qy 121 GAGCCCGAGGAAGATGTTGCTCAGGGAGGATCCTCAGCGCACCTCGGAGCTG 180	, 181	61 ProSerAbnLeuSerValPheThrSerTyrLeuAspLeuSerWetAbnAsnIleSerGln	QY 241 CTGCTCCCGAATCCCCTGCCCAGTCTCCTGGAGGAGTTACGTCTTGCGGGAAAC 300	Qy 301 GCTCTGACATACCTACCAAGGAGCATTCACTGGCCTTTACAGTCTTAAAGTTCTTATG 360	QY 361 CTGCAGAATAATCAGCTAAGACACGTACCCACAGAAGCTCTGCAGAATTTGCGAAGCCTT 420	Qy 421 CAATCCTGCGTCTGGATGCTAACCACATCAGCTATGTGCCCCCAAGCTGTTTCAGTGGC 480	Qy 481 CTGCATTCCCTGAGGCACCTGTGGCTGGATGACAATGCGTTAACAGAAATCCCCGTCCAG 540	Qy 541 GCTTTTAGAAGTTTATCGGCATTGCAAGCCATGACCTTGAACCAAAATACACCAC 600	Qy 601 ATACCAGACTATGCTTTGGAAACCTCTCCAGCTTGGTAGTTCTACATCTCCATAACAAT 660	AGAATCCACCCCTGGGAAAGAAATGCTTTGATGGGCTCCACAGCCTAGAGACTTTAGAT 	Qy 721 TTAAATTACAATAACCTTGATGAATTCCCCGCTGCAATTAGGACACTCTCCAACCTTAAA 780	Oy 781 GAACTAGGATTTCATAGCAACAATATCAGGTCGATACCTGAGAAAGCATTTGTAGGCAAC 840	Qy 841 CCTTCTTATTACATACATTTCTATGACAATCCCATCCAATTGTTGGTGGGATCTGCT 900
Qy 2341 CCTGTGGCTTTCTTGTCCTTTTAATAACCTTACATTTATCAGTCCTGAAGTA 2400 Db 781 ProValAlaPheLeuSerPheSerSerLeuIleAsnLeuThrPheIleSerProGluVal 800	Qy 2401 ATTAAGTTTATCCTTCTGGTAGTCCCACTTCCTGCATGTCTCAATCCCTTCTTAC 2460		UY 251 Itarakanantahanantahan 1980 	Qy 2581 TCCTGTGACTCAACTCTAGGAACCTTTACCAGCTCCAGCATCACTTATGACCTG 2640	Qy 2641 CCTCCCAGTTCCGTGCCATCACCAGCTTATCCAGTGACTGAGAGCTGCCATCTTTCCTCT 2700	Qy 2701 GTGCCATGTCTC 2721 Db 901 ValAlabeValProCysleu 907		US-10-295-027-1331 ; Sequence 1331, Application US/10295027 ; Publication No. US2003022350A1 ; GENERAL INFORMATION:	; APPLICANT: Aziz, Daniel ; APPLICANT: Aziz, Natasha ; APPLICANT: Ginsberg, Wendy M. ; APPLICANT: Gish, Kurt C.	<pre>; APPLICANT: Glynne, Richard ; APPLICANT: Hevezi, Peter A. ; APPLICANT: Mack, David H. ; APPLICANT: Murray, Richard</pre>	; APPLICANT: Watson, Susan R. ; APPLICANT: Bos Biotechnology, Inc. ; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and ; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer	; FILE REFERENCE: 0.18501-012500US; CURRENT APPLICATION NUMBER: US/10/295,027; CURRENT FILING DATE: 2002-11-13; PRIOR APPLICATION NUMBER: US 09/663,733	; PRIOR FILING DATE: 2000-09-15 ; PRIOR APPLICATION NUMBER: US 60/350,666 ; PRIOR FILING DATE: 2001-11-13 ; PRIOR APPLICATION NUMBER: US 60/335,394	; PRIOR FILING DATE: 2001-11-15 ; PRIOR APPLICATION NUMBER: US 60/332,464 ; PRIOR FILING DATE: 2001-11-21 ; PRIOR APPLICATION NUMBER: US 60/334,393	; PRIOR FILING DATE: 2001-11-29 ; PRIOR APPLICATION WUMBER: US 60/340,376 ; PRIOR FILING DATE: 2001-12-14 ; PRIOR APPLICATION NUMBER: US 60/347,211	PRIOR FILING DATE: 2002-01-08 PRIOR APPLICATION NUMBER: US 60/347,349 PRIOR PILING DATE: 2002-01-10 PRIOR APPLICATION NUMBER: US 60/355,250	; PRIOR FILING DATE: 2002-02-08 ; PRIOR APPLICATION NUMBER: US 60/356,714 ; PRIOR FILING DATE: 2002-02-13 ; Remaining Prior Application data removed - See File Wrapper or PALM.	; NUMBER OF SEQ ID NOS: 1386 ; SOFTWARE: PatentIn Ver. 2.1 ; SEQ ID NO 1331 ; LENGTH: 907

Qy 1981 GAGCGTGGGTTCTCTGTGAAATATTCTGCAAAATTTGAA 	Oy 2041 CTGAAAGTAATCATTTGCTCTGTGCCCTGCTGGCCTTG	Qy 2101 CTGGGTGGCAGCAAGTATGGCGCCTCCCCTCTCTGCCTG(2161	2221	2281	2341	Oy 2401 ATTANGTTTATCCTTCTGGTAGTCCACTTCCTGCACTTCTGCACTTCTTTTGCACTTCTGCACTTCTGCACTTCTGCACTTCTGCACTTCTTTCT	2461	2521	N C	2641 CCICCCAGIICCGIGCCAILA 	Oy 2701 GTGGCATTGTCCCATGTCTC 2721 	KESUL1 8 US-10-751-736-84 ; Sequence 84, Application US/10751736 ; Publication No. US20040265230A1	; APPLICANT: Myeth; APPLICANT: Martinez, Robert; APPLICANT: Martinez, Robert; APPLICANT: Martinez, Rugene	HITLE OF INVENTION: COMPOSITIONS AND METHODS FOR D ITILE OF INVENTION: CANCERS (031896-002000) FILE REFERENCE: AMJO0927 (031896-002000) CHERENCE: AMJO0927 (031896-002000)	CURRENT FILING DATE: 2003-01-06 PRIOR APPLICATION NUMBER: US Provisional Application PRIOR FILING DATE: 2003-01-06 NUMBER OF SEC IN NOS. 64873	SEQ ID NO 84 LENGTH: 907 TYPE: PRT
901 TITCAACATTTACCTGAACTAAGAACACTGACTCTGAATGGTGCCTCACAAATAACTGAA 960 	TITCCTGATTTAACTGGAACTGCAAACCTGGAGAGTCTGACTTTAACTGGAGGACACAGATC	TCATCTTCCTCCAAACCGTCTGCAATCAGTTACCTAATCTCCAAGTGCTAGATCTGTCT	TACAACCTATTAGAAGATTTACCCAGTTTTCAGCCAAAAGCTTCAGAAAATTGACTTCAGCCAAAAGCTTCAGAAAAATTGACTTCAGCCAAAAGCTTCAGAAAAATTGACTTCAGCCAAAAGCTCAGAAAAAAAA	CTAAGACATAATGAAATCTACGAAAT 	01 CGATCGCTGAATTTGGCTTGGAACAA 	TTGCCATCCCTAATAAAGCTGGACCT	1321 GGGTTACAFGGTTTAACTCACTTAAAATTAACAGGAAATCATGCCTTACAGAGCTTGATA 1380 	rcarcasaaactriccagaactcaaggriatagaaatgccriaigcriaccaggcrgriii	GCATTTGGAGTGTGTGAGAATGCCTA	1501 AGCAGTATGGACGTCTTCATAAGAAGATGCTGGAATGTTTCAGGCTCAAGATGAACGT 1560 	1561 GACCTTGAAGATTTCCTGCTTGACTTTGAGGAAGACCTGAAAGCCCTTCATTCA	1621 TGTTCACCTTCCCCAGGCCCCTTCAAACCCTGCTGGTTGATGGCTGGC	1681 AGAATTGGAGTGTGGACCATAGCAGTTCTGGCACTTACTT	1741 ACAGTITICAGAICCCCTCTGTACAITICCCCCATTAAACTGTTAATIGGGGTCATCGA 1800 	1801 GCAGTGAACATGCTCACGGGAGTCTCCAGTGCCGTGGTGGCTGGTGGATGCGTTCACT 1860 	1861 TTTGGCAGCTTTGCACGACATGGTGCCTGGTGGGAAATGGGGTTGGTT	1921 GGTTTTTTGTCCATTTTTGCTTCAGAATCATCTGTTTTCCTGCTTACTCTGGCAGCCCTG 1980
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Qy 901 TTTCAACATTTACCTGAACTAAGAACACTGACTGAATGGTGCCTCACAAATAACTGAA 960 Db 301 PheGlnHisLeuProGluLeuArgThrLeuThrLeuAshGlyAlaSerGlnIleThrGlu 320 Qy 961 TTTCCTGATTTAACTGGAACTGCAAACCTGGAGATCTGACTTTAACTGGAGCACAGATC 1020 Db 321 PheProAspLeuThrGlyThrAlaAshCeuGluSerLeuThrLeuThrGlyAlaGlnIle 340 Qy 1021 TCATCTTCCTCAAACCGTCTGCAATCAGTTACCTAATCTCCAAGTGCTAGATCTCT 1080 Db 341 SerSerLeuProGlnThrValcYsAsnGlnLeuProAsnLeuGlnYalLeuAspLeuSer 360	Qy 1081 TACAACCTATTAGAAGATTTACCCAGTTTTTCAGTCTGCCAAAAGCTTCAGAAAATTGAC 1140 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	1201 CGATCGCTGAATTTGGCAAAAATTGCTAATTATTCACCCCAATGCATTTTCCACT	Db 421 LeuProSerLeuTleLysLeuAspLeuSerSerAsnLeuLeuSerSerPheProIleThr 440 Qy 1321 GGGTTACATGGTTTAACTCACTTAAAATTAACAGGAAATCATGCCTTACAGAGCTTGATA 1380 Db 441 GlyLeuHisGlyLeuThrHisLeuLysLeuThrGlyAsnHisAlaLeuGlnSerLeuTle 460	1381 TCATCTGAAAACTTTCCAGAACTCAAGGTTATAGAAATGCCTTATGCTTACCAGTGCTGT 1	OY 1441 GCATTTGGACTGTGAGAATGCCTATAAGATTTCTAATCGAATAAAGGTGACAAC 1500		1621 TGTTCACCTTCCCAGGCCCCTTCAAACCCTGTGAACACCTGGTTGATGGCTGGTGATC	OY 1681 AGAATTGGAGTGTGGACCATAGCAGTTCTGGCACTTACTT		4 9	Qy 1921 GGTTTTTGCCTCATTTTGCTTCAGAATCATCTGTTTTCCTGCTACTCTGGCAGCCCTG 1980
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ORGANISM: Homo sapiens US-10-751-736-84 Homo sapiens US-10-751-736-84 Homo sapiens US-10-751-736-84 Homo sapiens US-10-751-736-81 Homo sapiens Us-10-751-736-81 Homo sapiens Us-10-751-736-81 Us-10-751-736-84 Us-907 Us-907	Qy 1 Argascaccrccascrcasrasacrccrasscaracacrasacrasacrascacc 60	Db 21 GlyGlySerSerProArgSerGlyValLeuLeuArgGlyCysProThrHisCysHisCys 40 121 GAGCCCGACGGCAGGATGTTGCTCAGGGTGGACTGCTCCGACCTGGGGTCTCTCGAGGTTG 180	61 ProSerAenLeuSerValPheThrSerTyrLeuAspLeuSerWetAenAsn1leSerGln 241 CTGCTCCCGAATCCCCTGCCCAGTCTCCTGGAGGAGTTACGTCTTGCGGAAAC [DO 81 Leuleurroasneroleurroserleuargrheleudiluleuargleualadijasn 100 Qy 301 GCTCTGACATACATTCCCAAGGGAGCATTCACTGGCCTTTACAGTCTTAAAGTTCTTATG 360	361 CTGCAGAATAATCAGCTAAGACACGTACCCACAGAAGCTCTGCAGAATTTGCGAAGCCTT	Qy 421 CAATCCCTGCTCTGGATGCTAACCACATCAGCTATCTGCCCCCAAGCTGTTTCAGTGGC 480 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Db 161 LeuHisSerLeuArgHisLeuTrpLeuAspAspAsnAlaLeuThrGluIleProValGin 180	Qy 601 ATACCAGACTATGCCTTTGGAAACCTCCAGGCTTGGTAGTTCTACATCTCCATAACAAT 660	Qy 661 AGAATCCACTCCCTGGGAAAGAATGCTTTGATGGGCTCCACAGCCTAGAGACTTTAGAT 720 Db 221 ArgileHisSerLeuGlyLysLysCysPheAspGlyLeuHisSerLeuGluThrLeuAsp 240 Qy 721 TTAAATTACAATAACCTTGATGAATTCCCCACTGCAATTAGGACACTCTCCAACCTTAAA 780	Db 241 LeuAsnTyrAsnAsnLeuAspGluPheProThrAlaileArgThrLeuSerAsnLeuIys 260 Qy 781 GAACTAGGATTTCATAGCAACAATATCAGGTCGATACCTGAGAAAGCATTTGTAGGCAAC 840 L	CCTTCTCTTATTACAATACATTTCTATGACAATCCCATCCAATTTGTTGGGAGATCTGCT 90

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Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 100.00\$ Indels: 0 DB: 17	US-10-751-736-21 (1-2724) x US-10-482-029-158 (1-907) QY	1 MECASPINISSEINISTATTATTATTATTATTATTATTATTATTATTATTATTAT	121 GAGCCCGACGGCAGGATGTTGCTCAGGGTGGACCTGCTCCGACCTGGGGCTCTCGGAGCTG 1	181 CCTTCCAACCTCTCACCTCCTAGACCTCAGTATGAACAACATCAGTCAG	CTGCTCCCGAATCCCCTGCCCAGTCTCCTGCAGGAGTTACGTCTGCGGGAAAC 3	301 GCTCTGACATACATTCCCAAGGGACCATTCACTGGCCTTTACAGTCTTAAGTTCTTATG 36	361 CTGCAGARTAATCAGCTAAGACACCTACCACAGAAGCTCTGCAGAATTTGCGAAGCTT 42 [Qy 421 CAATCCCTGCGTCTGGATGCTAACCACATCAGCTATGTGCCCCCAAGCTGTTTCACTGGC 480	Qy 481 CTGCATTCCCTGAGGCACCTGTGGCTGGATGACAANGCGTTAACAGAAATCCCCGTCCAG 540	Qy 541 GCTTTAGAAGTTTATCGCATTGCAAGCATGACCTTGGCCCTGAACAAAATACACCAC 600	Qy 601 ATACCACACTATGCCTTTGGAAACCTCTCCAGCTTGGTAGTTCTACATCTCCATAACAAT 660	Qy 661 AGAATCCACTCCCTGGGAAAGAATGCTTTGATGGCTCCACACGCCTAGAGACTTTAGAT 720	Qy 721 THAAATHACAATHACCTTGAATHACCTGGAATHAGGACACTCTCCAACCTTAAA 780 Db 241 LeuAsnfyrAsnAsnLeuAspGluPheProThrAlaileArgThrLeuSerAsnLeuJys 260	Qy 781 GAACTAGGATTTCATAGCAACAATATCAGGTCGATACCTGAGAAAGCATTTGTAGGCAAC 840	Qy 841 CCTTCTCTTATTACAATACATTTCTATGACAATCCCATCCAATTTGTTGGGAGATCTGCT 900	Qy 901 TITCAACAITTACCTGAACTAAGAACACTGACTCTGAATGGTGCCTCACAATAACTGAA 960	Qy 961 TITCCTGATTTAACTGCAAACCTGGAGAGTCTGACTTTAACTGGAGCACAGATC 1020
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Query M DB:	Match: 88.86% Indels: 2 14 Gaps: 0	& f	1021 TCATCTTCTTCTTCAAACCGTCTGCAATCAGTTACCTAATCTCCAAGTGCTAGATCTGTCT 1080
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US-10-751-736-21 (1-2724) x US-10-505-486-103 (1-1145)	Qy 1 AIGGACACCTCCCGGCTCGGTGTGCTCCTTGCCTGTGCTGCTGCTGC	Qy 61 GGGGCAGCTCTCCCAGGTCTGGTGTTGCTGAGGGGCTGCCCCACACACTGTCATTGC 120	Qy 121 GAGCCCGAGCAGGATGTTGCTCAGGAGGGGACCTGGGAGCTCTCGGAGCTG 180	Qy 181 CCTTCCAACCTCAGCGTCTTCACCTCCTACCTCAGTATGAACAACATCAGTCAG	Qy 241 CTGCTCCCGAATCCCCTGCCCAGTCTCCTGGAGGGTTACGTCTTGCGGGAAAC 300	Qy 301 GCTCTGACATACCCAAGGGAGCATTCACTGGCCTTTACAGTCTTAAGATTCTTATG 360	Oy 361 CTGCAGAATAATCAGCTAAGACACGTACCCACAGAAGCTCTGCAGAATTTGCGAAGCCTT 420	QY 421 CAATCCCTGCGTCTGGATGCTAACCACATCAGCTATGTGCCCCCAAGCTGTTTCAGTGGC 480	Qy 481 CTGCATTCCCTGAGGCACCTGTGGCTGGATGACAANGCGTTAACAGAAATCCCCGTCCAG 540	Qy 541 GCTTTTAGAAGTTTATCGGCATTGCAAGCCATGACCTGGCCCTGAACAAAATACCACA 600	Qy 601 ATACCAGACTATGGAAACCTCTCCAGCTTGGTAGTTCTACATCTCCATAACAAT 660	Qy 661 AGAATCCACTCCTGGGAAAGAATGCTTTGATGGGCTCCACAGCCTAGAGACTTTAGAT 720	Qy 721 TTAAATTACAATAACCTTGANGAATTCCCCACTGCAATTAGGACACCTCTCCAACCTTAAA 780	Qy 781 GAACTAGGATTTCATAGCAACAATATCAGGTCGATACCTGAGAAAAGCATTTGTAGGCAAC 840	Qy 841 CCTTCTTATTACAATACATTTCTATGACAATCCCATCCAATTTGTTGGGAGATCTGCT 900 L	GGTGCC GlyAla	TTAACTGGAACTGCAAACCTGGAGAGTCTGGACTTTAACTGGAGCACAGATC 1	CTAGATCTGTCT 10
	Oy 2161 AGCACCATGGGCTACATGGTCGCTCTTGCTCAATTCCCTTTGCTTCCTGATG 2220	QY 2221 ACCATTGCCTACACCAAGCTCTACTGCAATTTGGACAAGCAGACACTGGAGAATATTTGG 2280 DD 741 ThrileAlaTyrThrLysLeuTyrCysAsnLeuAspLysGlyAspLeuGluAsnIleTrp 760	OY 2281 GACTGCTCTAIGGT-AAACACATTGCCCTGTICACCACCTGCACTGCATCCTAAACTG 2339	OY 2340 CCCTGTGGCTTTCTTGTCCTCTTTAATAAACCTTACATTTATCAGTCCTGAAGT 2399 1	Qy 2400 AATTAAGTTTATCCTTCTGGTGGTAGTCCCACTTCCTGCATGTCTCAATCCCCTTCTGTA 2459	Oy 2460 CAICTIGITCAAICCTCACITTAAGGAACGAICTGGTGAGCCTGAGAAAGGAAACCTACGT 2519	OY . 2520 CTGGACAAGATCAAAACACCCAAGCTTGATGATTAACTCTGATGATGTCGAAAAACA 2579	Qy 2580 GTCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTTATGACCT 2639	QY 2640 GCCTCCCAGTTCCGTGCCATCACCAGCTTATCCAGTGACTGAGAGCTGCCATCTTTCCTC 2699	Oy 2700 TGTGGCATTTGTCCCATGTCTC 2721	RESULT 11 US-10-505-486-103 ; Sequence 103, Application US/10505486 ; Publication No. US2005011863921	GENERAL INFORMATION: APPLICANT: Takeda Chemical Industries, Ltd. TITLE OF INVENTION: Determination of a ligand PTIE PERPENDENT DETERMINATION	CURRENT APPLICATION NUMBER: US/10/505,486 CURRENT FILING DATE: 2004-08-20 PRICA PAPLICATION NUMBER: UP 2002-45728 PRICA FILING DATE: 2002-03-22	; PRIOR APPLICATION NUMBER: JP 2002-213949 ; PRIOR FILING DATE: 2002-07-23 ; PRIOR APPLICATION NUMBER: JP 2002-298237 ; PRIOR PTI, ING DATE: 2002-10-11	NUMBER OF SEQ ID NOS: 233 ; SEQ ID NO 103 ; LENGTH: 1145		 	

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RESULT 12

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Sequence 27, Application US/09970944

Sequence 27, Application No. US20030204052A1

GENERAL INFORMATION:

APPLICANT: Herrman, John L

APPLICANT: Rastelli, Luca

APPLICANT: Rastelli, Luca

APPLICANT: Shimkets, Richard A

TITLE OF INVENTION: No. US20030204052A1e1 Proteins and Nucleic Acids Encoding Same and TITLE OF INVENTION: No. US20030204052A1e1 Proteins

TITLE OF INVENTION: No. US20030204052A1e1 Proteins and Nucleic Acids Encoding Same and TITLE OF INVENTION: NUTUBER: US/09/970,944

CURRENT APPLICATION NUMBER: 60/237,862

PRIOR FILING DATE: 2000-10-04

NUMBER OF SEQ ID NOS: 62

SEQ ID NO 27

SEQ ID NO 27 an TGGACAAGATCAAAACACCCCAAGCTTGATGTCAATTAACTCTGATGATGTCGAAAAAACAG **PGCTTCCTCATGATG** GACTGCTCTATGGTAAAACACATTGCCCTGTTGCTCTTCACCAACTGCATCCTAAACTGC 2341 CCTGTGGCTTTCTTGTCCTTCTCCTTTAATAAACCTTACATTTATCAGTCCTGAAGTA TCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTTATGACCTG ProvalAlaPheLeuSerPheSerSerLeuIleAsnLeuThrPheIleSerProGluVal 816 0 1 2 2

1350 AACAGGAATCATGCCTTACAGAGCTTGATACTCTGAAAACTTTCCAGAACTCAAGGT	1830 TGCCGTGCTGGCTGGTGGATGCGTTCACTTTTGCAGGCTTTGCACGACATGGTGCCTG 1889 610 rAlaValLeuAlaGlyValAspAlaPheThrPheGlySerPheAlaArgHisGlyAlaTr 630 1890 GTGGGAGAATGGGTTGCTTGCTTTTTGTCCATTTTTGCTTCAGAATC 1949 [2070 GCTGGCCTTGACCATGGCCGCAGTTCCCCTGCTGGCTGGC
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- 그는 집_하 하느레 하느레 경그들 - 유청 그룹을 '무리를 가게 되었다'로 사람이 바로	830 Ouery 2549 DB: 2549 Oy-10- 850 Oy 2609 Db 870 Oy 2669 Db		Inc. Diagnosis of Cancer, Compositions and E Screening for Modulators of Cancer		11-15 R: US 60/332,464 QY R: US 60/334,393 11-29 R: US 60/340,376 R: US 60/347,211 Db R: US 60/347,213 CY	- See File Wrapper or PALM.	Length: 883 Matches: 621 Conservative: 0 Mismatches: 0

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APPLICANT: Eos Blotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR PELING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR PILING DATE: 2001-11-29
PRIOR PILING DATE: 2001-11-24
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR PILING DATE: 2002-11-04
PRIOR PILING DATE: 2002-01-10
PRIOR PILING DATE: 2002-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 HisPheTyrAspAsnProlleGlnPheValGlyArgSerAlaPheGlnHisLeuProGlu
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; ORGANISM: Homo sapiens
US-10-295-027-1330
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Best Local Similarity:
Query Match:
DB:
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                 CATGGTGCCTGGTGGGAGAATGGGGTTGGTTGCCATGTCATTGGTTTTTTTGTCCATTTTTT
                                                                                                                                                                                                     743 HislleAlaLeuLeuLeuLeuPheThrAsnCysIleLeuAsnCysProValAlaPheLeuSer
                                                                                                                                                                                                                                                                                                  2059 CTCTGTGCCCTGCCTTGACCATGGCCGCAGTTCCCCTGCTGGGTGGCAGCAAGTAT
                                          603 HisGlyAlaTrpTrpGluAsnGlyValGlyCySHisVallleGlyPheLeuSerllePhe
                                                                                                                                       623 AlaSerGluSerValPheLeuLeuThrLeuAlaAlaLeuGluArgGlyPheSerVal
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; Sequence 1330, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Afar, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glsh, Kurt C.
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Hack, David H.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
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Qy CTAAGAACACTGACTCTGAATGGTGCCTCAC	743 HislleAlaLeuLeuLheThrAsnCysIleLeuAsnCysProValAlaPheLeuSer 762	qg ,
Oy 859 CATTCTATGACAATCCCATCCAATTGTTG	LeulyILysasilleunspluysotyaspleuoitusilliteilpasplysotinetvallys CACATTGCCTGTTGCTTTCACCAACTGCATCCTAAACTGCCTGTGGCTTTCTTGTCC	3 &
10-173-9	2239 CTCTACTGCAATTTGGACAAGGGACCTGGAGAATATTTGGGACTGCTCTATGGTAAAA 2298 [ර් ස්
t Similarity: 100.00\$ ocal Similarity: 100.00\$ Match: 18		<i>&</i> 8
Alignment Scores: Pred. No.: Control Matches	2119 GGCGCTCCCCTCTGCCTGCCTTTGCCTTTTGGGGGGGCCCAGCACCATGGGCTACATG 2178	යි ර
; LENGTH: 883 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-173-999-28	2059 CTCTGTGCCCTGCTGGCCTTGACCATGGCCGCAGTTCCCCTGCTGGGTGGCAGCAAGTAT 2118 	ර් යි
; PRIOR FILING DATE: 2001-04-12; NUMBER OF SEQ ID NOS: 163; SOFTWARE: PatentIn Ver. 2.1; SEO ID NO 28	1999 AAATATTCTGCAAAATTTGAAACGAAAGCTCCATTTTCTAGCCTGAAAGTAATCATTTTG 2058 	යි සි
; PRIOR APPLICATION NUMBER: US 60/350,666; ; PRIOR PILING DATE: 2001-11-13; PRIOR APPLICATION NUMBER: US 60/372,246;		qq
FRIOR FILING DATE: 2001-04: PRIOR FILING DATE: 2001-08-27		8 8
CURRENT FILLING DATE: 2002-06-17 PRIOR APPLICATION NUMBER: US 60/299,234	1879 CATGGTGCCTGGTGGAAAGGGGGTTGCCCATGTCATTGTTTTTT 1938	රි ස
; TITLE OF INVENTION: and Methods of Screen; TITLE OF INVENTION: Cancer; HIER REFERENCE: 018501-002420US	1819 GGAGTCTCCAGTGCCGTGCTGGTGGGATGCGTTCACTTTTGGCAGCTTTGCACGA 1878 	& 8
APPLICANT: Mack, David H. APPLICANT: Gish, Kurt C. APPLICANT: Bos Blotechnology, Inc. TITE: POR INTENTION: Methods of Distinction	1759 CTGTACATTTCCCCCATTAAACTGTTAATTGGGGTCATCGCAGCAGTGAACATGCTCACG 1818 	\$ &
US-10-17-999-28 ; Sequence 28, Application US/10173999 ; Publication No. US20040005563A1	1699 ATAGCAGTTCTGGCACTTACTTGTAATGCTTTGGTGACTTCAACAGTTTTCAGATCCCT 1758 	යි ර
E===	1639 CCCTTCAAACCTGTGAACACCTGGTTGATGGCTGGCTGATCAGAATTGGAGTGTGGACC 1698 	& 4a
Db 863 SerProAlaTyrProValThrGluSerCysH	1579 CTTGACTTTGAGGAAGACCTGAAAGCCCTTCATTCAGTGCAGTGTTCACCTTCCCCGGGC 1638 	රු සි
2599 843	1519 CATAAGAAAGATGCTGGAATGTTTCAGGCTCAAGATGAACGTGACCTTGAAGATTTCCTG 1578 	ò a
2539 CCAAGCTTGAT 	1459 AATGCCTATAAGATTTCTAATCAATGGAATAAAGGTGACAACAGCAGTATGGACGACCTT 1518 	<i>&</i> 원
2479 803	1399 GAACTCAAGGTTATAGAAATGCCTTATGCTTACCAGTGCTGTGCATTTGGAGTGTGTGAG 1458 	& 8
2419 783	1339 CACTTAAAATTAACAGGAAATCATGCCTTACAGAGCTTGATATCATCTGAAAACTTTCCA 1398 	රු සි
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0 7	Oy 2359		ATAAACCTTACA1		TTCTCCTCTTTAATAAACCTTACATTTATCAGTCCTGAAGTAATTAAGTTTATCCTTCTG	2418
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a	Qy 2479		CTGGTGAGCCTG	AGAAAGCAAACCTAC	TTTAAGGAGGATCTGGTGAGCTGAGAAAGCAAACCTACGTCTGGACAAGATCAAAACAC	2538
Ω	Db 803		LeuValSerLeu?	ArgLysGlnThrTyr'	/alTrpThrArgSerLysHis	822
o	Qy 2539		TCAATTAACTCTC	SATGATGTCGAAAAA(CCAAGCTTGATGTCAATTAACTCTGATGATGTCGAAAAACAGTCCTGTGACTCAACTCAA	2598
Ω	Db 823		SerileAsnSer	AspAspValGluLys	31nSerCysAspSerThrG1n	842
O	Qy 2599		TTTACCAGCTCC	AGCATCACTTATGAC	GCCTIGGTAACCTTTACCAGCTCCAGCATCACTTATGACCTGCCTCCCAGTTCCGTGCCA	26
Ω	Db 843		PheThrsersers	serilerhrtyraspi	euProProSerServalPro	862
O	Oy 2659		CCAGTGACTGAG	AGCTGCCATCTTTCC	TCACCAGCTTATCCAGTGACTGAGAGCTGCCATCTTTCCTCTGGGCATTTGTCCCATGT	2718
Δ	Db 863		ProValThrGlus	serCysHisLeuSer:	servalAlaPhevalProCys	882
O A	Qy 2719 Db 883	CTC 2721 				
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¥ D .~	KESULI IS US-10-173-999 ; Sequence 28	-28 , Application	. US/10173999	NESOL1 13 US-10-173-999-28 ; Sequence 28, Application US/10173999		
	Publication	No. US200400	05563A1			
	APPLICANT:	Mack, David	н.			
	APPLICANT:	Gish, Kurt Eos Biotech	C. mology, Inc.			
• • •	TITLE OF I	NVENTION: Met	hods of Diagr	losis of Ovaria	Cancer, Compositions	m
•	TITLE OF I	NVENTION: CA	incer	. Tot furnishing		
	FILE REFER CURRENT AP	ENCE: 018501- PLICATION NUM	.0024200S IBER: US/10/17	73,999		
	CURRENT FI	LING DATE: 2	002-06-17	234		
	PRIOR FILI	NG DATE: 2001	-06-18	ָרְ י		
	PRIOR APPL	ICATION NUMBE NG DATE: 2001	IR: US 60/315, -08-27	, 287		
• ••	PRIOR APPL	ICATION NUMBE	IR; US 60/350,	,666		
	PRIOR FILI	NG DATE: 2001 ICATION NUMBE	11-13 R: US 60/372,	,246		
. •-	PRIOR FILI	NG DATE: 2001	-04-12			
	SOFTWARE:	PatentIn Ver.	2.1			
•••	SEQ ID NO 28	883				
D	; ORGANISM: US-10-173-999	ORGANISM: Homo sapiens 0-173-999-28	_			
∢ 0	Alignment Scores: Pred. No.:			Length:	883	
S	core:		1.00		621	
or on Ori		ty: arity:	100.00% 100.00% 68.47%	Conservative: Mismatches: Indels:	000	
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O I			AATCCCATCCAA?	rttgttgggagarct	CATTICTATICACAATCCCATCCAATTTGTTGGGGGGTCTGCTTTTCAACATTTACCTGAA	6 6
D)	Db 263		AsnProllegini	PhevalGlyargser	AlaPneGinhisieurrosiu	28
a	Qy 919		ACTCTGAATGGTC	SCCTCACAAATAACT	CTAAGAACACTGACTCTGAATGGTGCCTCACAAATAACTGAATTTCCTGATTTAACTGGA	978

July 13, 2005, ecs	ProPheLysProCysGluHisLeuLeuAspGlyTrpLeuIleArgIleGlyValTrpThr ATAGCAGTTCTGGCACTTACTTGTAATGCTGTGACTTCAACAGTTTTCAGATCCCCT	6 6 6 6 6 6 6 6 6 6 6
completed: July	ATAGCAGTTCTGGCACTTACTTGTAATGCTTTGGTGACTTCAACAGTTTTCAGATCCCCT	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
Qy 2719 CTC 2721 Db 883 Leu 883	CCCTTCAAACCCTGTGAACACCTGCTTGATGGCTGGCTGATCAGAATTGGAGTGTGGACC	දු දු
2659 TCAC 	CTTGACTTTGAGGAAGACCTGAAAGCCCTTCATTCAGTGCAGTGTTCACCTTCCCCAGGC	8 6
843	1519 CATAAGAAAGATGCTGGAATGTTTCAGGCTCAAGATGAACGTGACCTTGAAGATTTCCTG 1578 	중 염
2539 823	1459 AATGCCTATAAGATTTCTAATGAATGAAAGGGGGACAACAGCAGTATGGACGACCTT 1518 	8 6
2479	1399 GAACTCAAGGTTATAGAAATGCCTTATGCAGTGCTGTGCATTTGGAGTGTGTGAG 1458 	ያ ያ
	1339 CACTTAAAATTAACAGGAAATCATGCCTTACAGAGCTTGATATCATCTGAAAACTTTCCA 1398 	දු දු
763	CTGGACCTATCGTCCAACCTCCTGTCGTCTTTCCTATAACTGGGTTACATGGTTTAACT	රු පි
2299	AATTGCTATTATTCACCCCAATGCATTTTCCACTTTGCCATCCCTAATAAAG	රු පි
. 2239	1159 TACGAAATTAAAGTTGACACTTTCCAGCAGTTGCTTAGCCTCCGATCGCTGAATTTGGCT 1218 	දි දි
	1099 TTACCCAGITITITCAGICTGCCAAAAGCITCAGAAAATIGACCTAAGACATAATGAAATC 1158 	중 음
683	1039 GTCTGCAATCAGTTACCTAATCTCCAAGTGCTAGATCTGTCTTACAACCTATTAGAAGAT 1098 	B &
663	979 ACTGCAAACCTGGAGAGTCTGACTTTAACTGGAGCACAGATCTCATCTTCCTCAAACC 1038 	ያ ያ
Db 643 LysTyrSerAlaLysPheGluf		셤

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: July 12, 2005, 17:43:08 ; Search time 11588 Seconds (without alignments) 11390.405 Million cell updates/sec Title: Perfect score: 2724 Sequence: 2724 Scoring table: OLIGO_NUC Gapop 60.0 , Gapext 60.0 Searched: 4708233 segs, 24227607955 residues Word size : 0 Total number of hits satisfying chosen parameters: 9416466 Minimum DB seq length: 0 Maximum DB seq length: 200000000	Docessing: Listing: 1: 95-18-11. 95-18-11. 95-18-18-18-18-18-18-18-18-18-18-18-18-18-	11: 90-81:* 12: 90-87:* 13: 90-un:* 14: 90-vi:* 15: 90-vi:* 16: 90-vi:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES Result No. Score Match Length DB ID Description	1 2724 100.0 2724 6 CQ721366 CQ721366 Sequence 2 2724 100.0 2724 6 CQ76684 CQ76684 RA308745 CQ76684 Sequence 4 2724 100.0 2724 6 AR549136 AR549136 AR549136 Sequence 5 2724 100.0 2724 6 AR549136 AR549136 Sequence 6 2724 100.0 2880 6 AR658241 AR549136 Sequence 7 2724 100.0 2880 6 AR658241 RA569206 Homo sapi B 2724 100.0 4559 6 BD075815 BD075815 Gequence 9 2622 96.3 2724 6 RA308754 AR47625 Sequence 10 2571 94.4 2724 9 AR647625 AR398754 AR39875 Sequence 10 2571 94.4 2724 9 AR61444 BD135244 Novel mam ACC 12 1090 40.0 145165 9 ACC78860 ARC75399 Homo sapi B13 1019 37.4 4095 9 ACC75399 ARC75399 Homo sapi B42915 AR39876 ARC75399 Homo sapi B42915 AR6168 Sequence C 16 212 7.8 162004 9 ACC99116 BV208561 GPR49 209 BC550152 Sequence C 16 212 7.8 162004 9 ACC99116 BV208561 GPR49 209 BC550152 Sequence C 16 22 2 60 6 CC550152 Sequence C 16 212 7.8 16204 9 ACC95015 ACC9850152 Sequence C 16 22 2 60 6 CC550152 Sequence C 17 12 4.6 816 11 BV208561 GPR49 209 ACC136417 Rattus no

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KDAGMFQAQDGBDLEDPLLDFEEDLKALHSYQCSPSGPFKCEHLLDGWLIRIGWWT
IAVLAUTCNALVTSTVFREDBLYISPIKLIGVIAAVMLTGVSSAVLAGVDAFTFGSF
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VEKQSCDSTQALVTFTSSSITYDLPPSSVPFPYFESCHLSSVAFVPCL
                                                                                                            2880 bp . mRNA linear PRI 31-JUL-1998 protein-coupled receptor HG38 mRNA, complete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2880)
                                                                                                                                                                                                                                                                                                            McDonald,T., Wang,R., Bailey,W., Xie,G., Chen,F., Caskey,C.T. and
Liu,Q.
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E 7 (bases 1 to 2880)

AS McDonald, T., Wang, R., Bailey, W. and Liu, Q.

AL Submitted (29-APR-1998) Human Genetics, Merck Research Labs, West Point, PA 19486, USA

ES Location/Qualifiers

Ource /organism="Homo sapiens"

/mol type="mRNA"

/db_ref="taxon:9606"

/chromosome="12"

/map="12q22-q23"

/map="12q22-q23"
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Matches 2724; Conservative 0
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G protein-coupled glycoprotein hormone receptor HG38.
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          TGGACAAGATCAAAACACCCCAAGCTTGATGTCAATTAACTCTGATGATGTCGAAAAACAG
                                                                                                                ATCTTGTTCAATCCTCACTTTAAGGAGGATCTGGTGAGCCTGAGAAAGCAAACCTACGTC
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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                                                                      GGGTTACATGGTTTAACTCACTTAAAATTAACAGGAAATCATGCCTTACAGAGCTTGATA
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	RESULT 9 AR308754 LOCUS DEFINITION Sequence 277 from patent US 6555339. ACCESSION AR308754 VERSION AR308754. GI:31700283 KEYWORDS SOURCE Unknown. ORGANISM Unknown. Unclassified. AUTHORS Liaw, C. W., Behan, D. P. and Chalmers, D. T. TITLE Non-endogenous, constitutively activated human protein-coupled receptors JOURNAL Patent: US 655539-A 277 29-APR-2003; FATURES SOURCE JOURNAL Patent: US 65539-A 277 29-APR-2003; FATURES ACCESSION AR308754 AD308754 AD308755 AD30875 AD3	Ouery Match
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Bukaryota, Matheria; Primates; Catarrhini; Hominidae; Homo.

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Burdh, D. M., Adams C., Adlo-Guolab B., Ali-coman, F.,

Barton, J., Bimage, M., Brown, E., Brown, M., Banks, T., Banck, T.,

Burch, P., Burket, C., Corle, Barnell, K.L., Banks, T., Banck, T.,

Burch, P., Burket, C., Corle, Burchli, K.L., David, N.C., Carron, T.F.,

Cartor, C., Corle, D. Dathorne, S. R., David, R. Davida, M.L., Davis, C.,

Cox, C., Corle, D., Dathorne, S. R., David, R. Davida, M.L., Davis, C.,

Davy-Carroll, L., Dedrich, D.A., Delaney, K.R., Delgado, O.,

Davy-Carroll, L., Poster, P., Franhart, C., Edgar, D., Edwards, C.,

Flaggy, N., Foot, J., Foster, P., Franta, P., Gabis, M., Garcia, A., Garner, T., Garza, M., Garner, T., Garza, M., Garner, T., Garza, M., Garner, T., Garza, M., Garner, M., Havlak, P., Hale, S., Hamilton, K., Han, J., Harlak, P., Hale, S., Hamilton, K., Han, J., Harlak, P., Hale, S., Hamilton, K., Han, J., Harnis, K., Hart, M., Havlak, P., Marlah, M., Londer, M., Loulesged, L., J., Lohtarge, C., Hollins, B., Homai, F.,

Martinda, B., Martinda, B., Martine, M., Loucier, R., Louse, L., Loulesged, L., Lottarge, C., Hollins, B., Homai, R., Martinda, M., Marten, M., Marting, B., Home, J., Indiarge, C., Luna, M., Miner, G., Mitchell, T., Martin, R., Martinda, A., Matchell, M., Moward, S., Moter, M., Mortie, S., Moter, M., Mortie, S., Moter, M., Mortie, S., Moter, M., Moter, M., Moter, M., Martinger, B., Home, J., Martinda, B., Home, J., Martinda, M., Mathingo, M., Modern, S., Moter, M., Palker, M., Mathingon, M., Moder, M., Ren, Y., Mallan, M., Mathington, M., Moder, M., Thomas, M., Thomas,
                                                                                                                                                                                                                                                                                      AC078860 145165 bp DNA linear PRI 23-JAN-2003
Homo sapiens 12 BAC RPI1-186F10 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
1999 CCTCCCCAGTTCCGTGCCATCACCAGCTTATCCAGTGACTGAGAGCTGCCATCTTTCCTCT 2058
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                                                                                                                         2059 GIGGCATTTGTCCCATGTCTCTAA 2082
                                                                                       2701 GIGGCATITGICCCATGICTCIAA 2724
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Submitted (31-MAR-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                    Submitted (01-APR-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 145165)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (15-WAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Worley, K.C.
Worley, K.C.
Direct Submission
Submitted (23-JAN-2003) Human Genome Sequencing Center, Departmen Submitted (23-JAN-2003) Human Genetics, Baylor College of Medicine, One Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Director Plaza, Houston, TX 77030, USA
On Mar 31, 2001 Lhis sequence version replaced gi:13324671.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                             (bases 1 to 145165)
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Peatures listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and

local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST Genes and Region of sequence similarity are identified by LAST Genes and Region of sequence similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found

http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

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144455
5.28339e-05
0.0137759
                 145169
Summary Statistics ------
                                                          Average error rate (BCM-Phrap estimate):
                                                                               than 40
                                                                                                  Number of consensus changing edits:
Number of N's in consensus :
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Edited+Context Consensus changing edits

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ttteggetea (c) tgeaacetec
aaaacacaca (a) caatagataa
ttgtattgca (a) atggetett
ttttttattt (t) tatagttaat
ttatteattt (t) tatagttaat
tetetetea (g) aaagaaaaga
aatggettt (a) aaatgggece
cttagactgt (g) aaagaaaaga
aatggetttt (a) aaatgggece
cttagactgt (g) aaagteagga
gctaatttt (a) aattegggt
cacatgcatt (a) ggtatttgt
cacatgcatt (g) agggaatget
gcttacacta (g) agggaatget
gcttacacta (g) aggaatget
gcttacacta (g) aggaatget
gctacacta (g) aggaatgaac
agatggtt (g) gcacttaat
aaatattgtc (c) taaataaagt
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                                      atcgttattg (n) tgttaattit
tttttattt (n) tatagttaat
tcatgaccta (n) tatagtcact
ctatctctac (n) aaagaaaaga
aatggcttt (g) aaatgggcc
cttagactgt (n) aatgtcagga
gctaatttt (n) cattttagt
cacatgatt (n) gatattgtc
tcaagcttg (n) atttcaggt
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 agatgtggat (a) gctgtggctt
tttcggctca (n) tgcaacctcc
aaaacaacat (n) caatagataa
ttgtattgca (n) atggcatctt
                                                                                                                            cagatcatct (n) agggaatgct
gcttacacta (n) aaaatgaacc
agcatggtgt (n) nncacttaat
                                                                                                                                                        gcatggtgtn (n) ncacttaata
catggtgtnn (n) cacttaataa
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/clone="RP11-186F10"
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complement (1740. .2021)
/rpt_family="AluJb"
complement (2098. .2151)
/rpt_family="LIMEc"
complement (2152. .2449)
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PF 05-FEB-1999 JP 1999029120
PR 06-FEB-1998 EP 98203157.6,27-JUL-1998 EP 98202519.9, PR 24-SEP-1998 EP 982031313.8
I YUDELSU CHRISTIAN HEIXOPU, PETORIYUSU JOHANNES VAN DEL SUPEKKU PC CI2N15/09,A61K38/00,A61P15/08,A61P43/00,C07K14/72,C12N1/15, PC
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PC C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/15,G01N33/50, PC
G01N33/566,
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CTGCAGAATAATCAGCTAAGACACGTACCCACAGAAGCTCTGCAGAATTTGCGAAGCCTT
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Heikopu,Y.C. and Supekku,P.J.V.D.
Novel ganadotropin receptor
Patent: JP 2000125884-A 3 09-MAY-2000;
AKZO NOBEL NV
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Novel gonadotropin receptor.
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                                                                                                                                                                                                                                                                                                                                                                     Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass sequencing, clone selection and full insert sequencing: Helix Research Institute (supported by Japan Key Technology Center etc.); cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center.
                                  775399 4095 bp mRNA linear PRI 03-SEP-2002 no sapiens cDNA PSEC0089 fis, clone PLACE1001148, highly similar Homo sapiens orphan G protein-coupled receptor HG38 mRNA.
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/mol_type="mRNA"
/db_xref="teaxon:9606"
/db_ref="teaxon:9606"
/clone="PLACE1001148"
/clone_Tib="PLACE1"
/clone_Tib="PLACE1"
/note="cloning vector: pME18SFL3"
/note="This 284 bases segment is not present in AF062006
and AF061444, probably caused by alternative splicing"
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                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T.,
Nakamura,Y., Sato,H., Nagahari,K., Sugano,S. and Isogai,T.
HRI human cDNA sequencing project
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Pred. No. 0;
0; Mismatches 1; Indels 0;
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AK075399.1 GI:22761463
oligo capping; fis (full insert sequence)
                                      AK075399
Homo sapiens cDNA PSEC0089 fis,
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99.9%;
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Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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C12N15/00,A61K37/02,C12N5/00
Strandedness: Single;
Topology: Linear;
Key
                                                                              1. .606
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Sequence 3 from Patent EP0950711.
AX016185
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                                                                                                                                                                                                                                                                                        Query Match 22.2%; Score 606; DB 6; Length 606; Best Local Similarity 100.0%; Pred. No. 2.9e-294; Matches 606; Conservative 0; Mismatches 0; Indels
Heikoop, J.C. and Van Der Spek, P.J.
Gonadotropin receptor
Patent: EP 9050711-A 3 20-OCT-1999,
AKZO NOBEL NV (NL)
Location/Qualifiers
                                                                                                                                  1. .606
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Post-processing: Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ع			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
-	2724	100.0	2724		AAA30770	Aaa30770 Human G p
7	2724	100.0	2724	8	ABZ42816	Abz42816 Human G p
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4	2724	100.0	2724	70	ADH14255	Adh14255 Human HG3
ß	2724	100.0	2724	12	ADI32985	Adi32985 Human G p
9	2724	100.0	2724	12	AD029923	Ado29923 Human GPC
7	2724	100.0	2880	11	ADN39796	Adn39796 Cancer/an
80	2724	100.0	2880	13	ADQ80249	Adq80249 G protein
σ	2724	100.0	2973	13	ADR67869	Adr67869 Human HG3
10	2724	100.0	3032	11	ADN39627	Adn39627 Cancer/an
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12	2724	100.0	4558	N	AAX23980	Aax23980 Human HG3
13	2724	100.0	4570	12	ADL12472	Adl12472 Human ste
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16	2622	96.3	2724	10	ADC22796	Adc22796 Human G p
17	2622	96.3	2724	10	ADH14269	Adh14269 Mutated h
18	2603	95.6	3297	7	AAX23981	Aax23981 Human HG3
19	1864	68.4	2651	10	ADB80463	Adb80463 Ovarian c
20	1864	68.4	. 2651	11	ADN39165	Adn39165 Cancer/an

Adn39795 Cancer/an	Aaz25344 Human LGR	Aca04772 cDNA enco	Abq55077 Human ova	Aaz40459 Human gon	Aba09697 Human bon	Abn47039 Human spl	Ado30213 Mouse GPC	Adr67870 Mouse HG3	Adi32988 5'FAM and	Aaa30768 Human G p	Adc22780 Human G p	Adh14253 Human HG3	Aaa30767 Human G p	Adc22779 Human G p	Adhl4252 Human HG3	Aai67921 Mouse LGR	Adn02241 Mouse CDS	Adk19406 ORF of cD	Aai67920 Mouse LGR	Adn02239 Mouse cDN	Adk19404 cDNA enco	Aax23973 Human HG3	Aax23974 Human HG3	Aax23972 Human HG3
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ALIGNMENTS

RESULT 1

G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug screening; agonist; Human G protein-coupled receptor HG38 cDNA. Behan DP, Chalmers DT, Liaw CW; AAA30770 standard; cDNA; 2724 BP. 99WO-US023938. 98US-00170496. (first entry) (AREN-) ARENA PHARM INC. antagonist; ss. WO200022129-A1. Homo sapiens. 12-OCT-1999; 13-OCT-1998; 21-AUG-2000 20-APR-2000. AAA30770; AAA30770

WPI; 2000-329165/28. P-PSDB; AAY90682.

Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical agents.

Example 1; Page 315-317; 341pp; English.

The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743 and AAA30775-A30779). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,

is substituted for an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous proline in TM6 to form a sequence X- (AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 camino acid structch between the substituted amino acid and the Pro may be endogenous, non-endogenous, or a mixture of endogenous and non-endogenous residues. The constitutively active GPCRs are useful for identifying catagonists, agonists and partial agonists per pharmaceutical agonists. The mutant proteins are also useful in research settings for elucidating the roles of the receptors in normal and diseased conditions. Antagonists for a particular GPCR are useful for treating for Antagonists for a particular GPCR are useful for recenting of disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous ligands. The present sequence represents cDNA encoding a human wild-type GPCR used in an expense compounds without the need for endogenous ligands. The present sequence represents cDNA encoding a human wild-type GPCR used in an expected to site-directed mutagenesis (SDM) to generate DNA encoding the corresponding mutant of the invention \$

Sequence 2724 BP; 665 A; 723 C; 554 G; 782 T; 0 U; 0 Other;

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ờ	721	TTAAATTACAATAACCTTGAATTCCCCACTGCAATTAGGACACTCTCCAACCTTAAA 780
οp	721	TTAAATTACAATAACCTTGATGAATTCCCCACTGCAATTAGGACACTCTCCAACCTTAAA 780
ò	781	
QQ	781	GAACTAGGATTICATAGCAACAATATCAGGICGATACCIGAGAAAGCATTIGTAGGCAAC 840
à ·	841	
q	841	CCTTCTCTTATTACAATACATTTCTATGACAATCCCATCCAATTTGTTGGGAGATCTGCT 900
ò	901	TITCAACAITTACCIGAACIAAAAACACIGACICIGAAIGGIGCCICACAAATAACIGAA 960
qq	901	TITCAACATTIACCTGAACTAAGAACACTGACTCTGAATGGTGCCTCACAAATAACTGAA 960
ò	961	
рр	961	TTTCCTGATTTAACTGGAACTGCAAACCTGGAGAGTCTGACTTTAACTGGAGCACAGATC 1020
ć	1021	TCATCTCTCCTCAAACCGTCTGCAATCAGTTACCTAATCTCCAAGTGCTAGATCTT
qq	1021	rearcretaracererecaricarracerarecearetecragicareterer 1080
ò	1081	TACAACCTATTAGAAGATTTACCCAGTTTTTCAGTCTGCCAAAAGCTTCAGAAAATTGAC 1140
Ωp	1081	TACAACCTATTAGAAGATTTACCCAGTTTTTCAGTCTGCCAAAAGCTTCAGAAAATTGAC 1140
δ	1141	CTAAGACAINATGAAATCTACGAAATTAAAGTTGACACTTTCCAGCAGTTGCTTAGCCTC 1200
Ωp	1141	CTAAGACATAATGAAATCTACGAAATTAAAGTTGACACTTTCCAGCAGTTGCTTAGCCTC 1200
ò	1201	CGAICGCIGAAITIIGGCIIGGAACAAAITGCIAITAITCACCCCAAIGCAITITCCACI 1260
qa	1201	CGATCGCTGAATTTGGCTTGGAACAAAATTGCTATTATTCACCCCAATGCATTTTCCACT 1260
È	1261	TIGCCATCCCTAATAAAGCTGGACCTATCGTCCAACCTCCTGTCGTCTTTTCCTATAACT 1320
qq	1261	TIGCCATCCCTAATAAAGCTGGACCTATCGTCCAACCTCCTGTCTTTTCCTATAACT 1320
Š	1321	GGGTTACATGGTTTAACTCACTTAAAATTAACAGGAAATCATGCCTTACAGAGCTTGATA 1380
qa	1321	GGGTTACATGGTTTAACTCACTTAAAATTAACAGGAAATCATGCCTTACAGAGCTTGATA 1380
ò	1381	TCATCTGAAAACTTTCCAGAACTCAAGGTTATAGAAATGCCTTATGCTTACCAGTGCTGT 1440
qq	1381	rcaictgaaaactitccagaactcaaggitalagaaargcctratgcttaccagrigit 1440
ò	1441	GCATITIGGAGTGTGTGAGAATGCCTATAAGATTTCTAATCAATGGAATAAAGGTGACAAC 1500
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ò	1561	GACCTIGAAGATITCCTGCTIGACTITIGAGAAGACCTGAAAGCCCTITCATICAGTGCAG 1620
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QQ	1621	
δ	1681	
qq	1681	AGAATTGGAGTGTGGACCATAGCAGTTCTGGCACTTACTT
ķ	1741	
Db	1741	

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Human G protein-coupled receptor GPR49 nucleotide SEQ ID NO:421.
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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino caids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or articular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for disquesting and designing drugs for capresence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for disquesting and designing drugs for capresence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for disquesting and designing drugs for caprestion immune-related diseases, immunological-related cell proliferative diseases, or autoimmune diseases, eg. ALDS, Alzheimer's disease, atherosclerosis, bacterial, fungal protozoan or viral infections, atherosclerosis, bacterial, fungal protozoan or viral infections, alternation, allergies, Crohn's disease, graft versus host disease, parkinson's disease, multiple sclerosis, pain, psoriasis, cancer, cardiomyopathy, chronic and acute cinflammation, allergies, Crohn's disease, graft versus host disease, pspilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorders, rheumatoid arthritis, trauma, ulcers, or any other minmunoassays and immunodiagnosis, and antibodies may be used in immunoassays and immunodiagnosis, and and antibodies may be used in immunoassays and immunodiagnosis, and antibodies may be exemplification of the present invention G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; call regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; pain; psoriasis; anxiety; depression; schlizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypertension; renal disorder; rheumatoid arthritis; trauma; New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or Gaps ö Sequence 2724 BP; 665 A; 723 C; 554 G; 782 T; 0 U; 0 Other; Indela DB 8; Score 2724; I Pred. No. 0; 0; Mismatches Disclosure; Fig 1; 523pp; English. (LIFE-) LIFESPAN BIOSCIENCES INC. Brown JP; ö 19-DEC-2001; 2001WO-US050107. 19-DEC-2000; 2000US-0257144P. 100.08; Best Local Similarity 100. Matches 2724; Conservative Roush CL, WPI; 2003-046718/04. P-PSDB; ABP81968. autoimmune diseases. WO200261087-A2 Homo sapiens. ulcer; gene; 08-AUG-2002. Burmer GC, Query Match ઠે

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(first entry)

04-MAR-2003

ABZ42816;

ABZ42816 ID ABZ4 XX AC ABZ4 XX DT 04-M

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transmembrane-6 region; TM6; intracellular-3 region; IC3.
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constitutively active version of an endogenous human G protein-coupled receptor (GPCR) that has a transmembrane-6 (TM6) region and an intracellular-3 (IC3) region, by substituting a specific amino acid in the TM6 region with a different amino acid, and testing for constitutive contitutive. The method is useful for creating a constitutively active version of an endogenous human GPCR that comprises a transmembrane 6 region and an intracellular loop 3 region. The altered human GPCR polypeptides are useful for screening test compounds for identification of inverse agonists or partial agonists of GPCR polypeptides, which may have therapeutic uses. The altered GPCRs may also be used to oreate a transment and encoding the altered GPCR. The method allows screening for compounds that medulate the activity of human G protein-coupled receptor without the need for provision of a ligand for the receptor. This is particularly useful in allowing currently known. This sequence represents for which no ligand is currently known. This sequence represents colva human GPCR.
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                                                            invention relates to a method for treating a non-endogenous,
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                                                                                                                                  human; non-endogenous; G protein-coupled receptor; GPCR;
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98US-0095677P.
98US-00170496.
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Best Local Similarity 100.0%;
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(BEHA/) BEHAN D P.
(CHAL/) CHALMERS D
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                                                                            Human HG38 cDNA
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13-OCT-1998;
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New antisense oligonucleotide comprising a sequence targeted to a nucleic acid encoding G protein-coupled receptor 49, useful for preparing a composition for treating e.g., neural or endocrine system disorder.
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                  TGGACAAGATCAAAAACACCCCAAGCTTGATGTCAATTAACTCTGATGATGTCGAAAAAAAGA
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                                                                   TCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTTATGACCTG
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endocrine system disorder; gene therapy; antisense therapy; human;
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GACTGCTCTATGGTAAAACACATTGCCCTGTTGCTCTTCACCAACTGCATCCTAAACTGC
                            GACTGCTCTATGGTAAAACACATTGCCCTGTTGCTCTTCACCAACTGCATCCTAAACTGC
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09-APR-2003; 2003US-0461329P,
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The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR polyerising several mice, each of which has a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgene or in an endogenous GPCR gene; cells derived of the GPCR polyerising several mice, each of which has a mutation in a different GPCR polynucleotides of the invention. The comprising a GPCR mucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzahimer's disease, distractions, disorders of the colon or intestine disorders of the adrenal gland; disorders of the colon or intestine syndroms; s disease, diarrhoea, food poisoning or irritable bowel syndroms; crown such a disorders (e.g., angina, cardiac arrhythmia or myccardial infarction); muscular disorders (e.g., autoimmune disorders (e.g., angina, cardiac arrhythmia or mycardial); immune disorders; (e.g., autoimmune disorders (e.g., angina, cardiac, arrhythmia or mycardial); immune disorders; (e.g., autoimmune disorders (e.g., angina, proster, cardiciency-related diseases or vitamin deficiency-related diseases); and disorders of the kidney, liver, lung, breast, ovary, unerus, prostate, testis, skin, stomach, pancreas, spleen, thymus and cuerus, prostate, testis, skin, stomach, pancreas, spleen, thymus and mycleic acid of the invention. Note: The fill sequence data for this cardiac acid of the present esquence represents a GPCR encocading the present comment of the prince of the proper of the present
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                                                                                              Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina pectoris, Parkinson's disease.
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Pavlova MN, Vassilatis D,
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Matches 2724; Conservative 0
  Mcilwain KL,
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Best Local Similarity
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  Madisen L,
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420	TCATTGT 480 CCGTCCAG 540 CCGTCCAG 540 CCGTCCAG 540	GCTTTTAGAAGTTTATCGGCATTGCAAGCCATGACCTTGGCCCTGAACAAAATACACCAC 600	. 660 . 660	720	780	840	006	096	1020	1080	1140	1200.	1260	TTGCCATCCTAATAAAGCTGGACCTATCGTCCAACCTCCTGTCGTCTTTTCCTATAACT 1320	GGGTTACATGGTTTAACTCACTTAAAATTTAACAGGAATCATGCCTTACAGAGCTTGATA 1380 	1440 1440	

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SEQ ID NO C168; 1385pp; English.
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                                                                                                                                                                                                                                              Human, differential expression; cancer; angiogenic disorder;
fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
                                                                 TCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTTATGACCTG
                                        TCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTTATGACCTG
                                                                                                                                                                                                                                                              inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnoslis; prognoslis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
                                                                                                                                                                                                                           Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C168
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3, Zlotnik
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Wilson KE,
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13-DEC-2001; 2001US-0335394P.
14-JDAN-2002; 2001US-0347319P.
16-JDAN-2002; 2002US-0347349P.
16-FEB-2002; 2002US-0355250P.
13-FEB-2002; 2002US-0355250P.
13-FEB-2002; 2002US-0356714P.
29-MAR-2002; 2002US-0356917P.
29-MAR-2002; 2002US-0370110P.
12-APR-2002; 2002US-0370110P.
15-JUL-2002; 2002US-0396819P.
16-JUL-2002; 2002US-0396819P.
22-JUL-2002; 2002US-0396819P.
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R, Watson SR,
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2001US-0332464P.
2001US-0334393P.
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09-SEP-2002; 2002US-0409450P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murray
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whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The cucleic acid of the invention, antibodies which specifically bind a cucleic acid of the invention, antibodies which specifically bind a cucleic acid of the invention, use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atterosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistaion syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a nucleic acid sequence of the invention.
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invention relates to nucleic acids and proteins (ADN38683-ADN40064)
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<i>≿</i> 8	721 TTAAATTACAATAACCTTGATGAATTCCCCACTGCAATTAGGACACTCTCCAACCTTAAA 780 	Qy 1801 GCAGTGAACATG Db 1849 GCAGTGAACATG	GCAGTGAACATGCTCACGGGAGTCTCCAGTGCCGTGCTGGTGGGTG
ò 6	GAACTAGGATTTCATAGCAACAATATCAGGTCGATACCTGAGAAAGCATTTGTAGGCAAC 84	Oy 1861 TTTGGCAGCTTT 	CAGCTTTGCACGACATGGTGCCTGGTGGGGAAAGGGGTTGGTT
8 8 8	CCTTCTCTATTACATACATTTCTATCACATCCCATCCAT	Qy 1921 GGTTTTTTGTCC	GITITITGCCATITITGCTTCAGAATCATCTGFTTTCCTGCTTACTCTGGCAGCCCTG 1980
8 %	TTTCAACATTTACCTGAACTAAGAACACTGACTCTGAATGGTGCTCCACAAATAACTGAA 96	Oy 1981 GAGCGTGGGTTC	GAGCGTGGGTTCTCTGTGAATATTCTGCAAAATTTGAAACGAAAGCTCCATTTTCTAGC 2040
දු පු	TTTCCTGATTTAACTGGAACTGCAACCTGGAGAGTCTGACTTTAACTGGACCAGATC 102	Oy 2041 CTGAAAGTAATC Db 2089 CTGAAAGTAATC	CTGAAAGTAATCATTTTGCTCTGTGCCCTGCTGGCCTTGACCATGGCCGCAGTTCCCCTG 2100
& 8	TCATCTCTTCCTCAACCGTCTGCAATCAGTTACCTAATCTCCCAAGTGCTAGATCTGTCT 108	Oy 2101 CTGGGTGGCAGC 	CTGGGTGGCAGCAAGTATGGCGCCTCCCTCTCTGCCTTTGCCTTTTGGGGAGCCC 2160
8 & 8	TACAACCTATTAGAACATTTACCCAGTTTTTCAGTCTGCCAAAAGCTTCAGAAAATTGAC 114	2161	AGCACCATGGGCTACATGGTCGCTCTCATCTTGCTCAATTCCCTTTGCTTCCTCATGATG 2220
& 43	CTAAGACATAATGAAATCTACGAAATTAAAGTTGACACTTTCCAGCAGTTGCTTAGCCTC 120	Qy 2221 ACCATTGCCTAC 	ACCATTGCCTACACCAAGCTCTACTGCAATTTGGACAAGGAGACCTGGAGAATATTTGG 2280
, 8 8	CGATCGCTGAATTTGGCTTGGAACAAAATTGCTATTATTCACCCCAATGCATTTTCCACT 126	Qy 2281 GACTGCTCTATG 	23
è 8	TTGCCATCCCTAATAAACTGGACCTATCGTCCAACCTCCTGTCGTCGTTTTCCTATAACT	2341	2 2
& 8	1321 GGGTTACATGGTTTAACTCACTTAAAATTAACAGGAAATCATGCCTTACAGAGCTTGATA 1380 	Qy 2401 ATTAAGTTTATC Db 2449 ATTAAGTTTATC	ATTAAGTTTATCCTTCTGGTAGTCCCACTTCCTGCATGTCTCAATCCCCTTCTGTAC 2460
\chi_{\text{8}}	TCATCTGAAAACTTTCCAGAACTCAAGGTTATAGAAATGCCTTATGCTTACCAGTGCTGT 144	Oy 2461 ATCTTGTTCAATO DD 2509 ATCTTGTTCAATO	ATCTTGTTCAATCCTCACTTTAAGGAGGATCTGGTGAGCCTGAGAAAGCAAACCTACGTC 2520
\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	GCATTTGGAGTGTGTGAGAATGCCTATAAGATTTCTAATGAATG	21	258
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දු පු	GCAG GCAG	2641	
රු සි	1621 TGTTCACCTTCCCCAGGCCCCTTCAAACCCTGTGAACACCTGCTTGATGGCTGGTTGT 1680 	Oy 2701 GTGGCATTGTCCCATGTCTCTAA	
දු දු	1681 AGAATTGGAGTGTGGACCATAGCAGTTCTGGCACTTACTT	RESULT 8 ADQ80249 ID ADQ80249 standard; cDNA	та, 2880 ВР.
& g	1741 ACAGITITCAGATCCCCTCTGTACATTTCCCCCATTAAACTGTTAATTGGGGTCATCGCA 1800 	XX AC ADQ80249; XX DT 21-OCT-2004 (first en'	ıtry)

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CTGCATTCCCTGAGGCACCTGTGGCTGGATGACAATGCGTTAACAGAAATCCCCGTCCAG
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                                       ss; gene; cytostatic; epidermal growth factor receptor modulator; identification; therapeutic response; cancer; EGFR; biomarker.
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     protein-coupled receptor 49 cDNA
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Matches 2724; Conservative
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This sequence encodes the human G protein-coupled receptor (GPCR) known as HG38. The HG38 protein and corresponding nucleic acid, may be used in the method of the invention for detecting colon or lung cancer. The first method involves performing an assay to determine the amount of HG38 in a sample of colon or lung tissue, and comparing the amount of protein to standard, thus detecting expression of protein in sample, where the tender of protein in sample where compression of protein in sample where it candard is diagnostic of colon or lung cancer. The second method involves hybridizing a composition comprising the HG38 coding sequence, or its complement, and a labelling moiety, to nucleic acids of a sample of colon or lung tissue under conditions to form at least one hybridization complex, detecting hybridization complex formation, and comparing complex formation to a standard, where the comparison reflects differential expression of the polynuclectide in the sample relative to the standard and is diagnostic of a colon or lung cancer. This first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene; human ; G protein-coupled receptor ; GPCR; HG38; colon ; lung
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                                                                                                                                                                                                                                                                                                          Location/Qualifiers
18. .2741
/*tag= a
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Human HG38 coding sequence.

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Detecting colon or lung cancer, PP

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method enables earlier diagnosis before the patient is symptomatic. Anti-
HG38 antibodies are useful for treating colon or lung cancer.
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                                  Sequence 2973 BP; 757 A; 759 C; 607 G; 850 T; 0 U; 0 Other;
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Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
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2, Watson SR,
           13-NOV-2001; 2001US-0350666P.
21-NOV-2001; 2001US-0332464P.
23-NOV-2001; 2001US-0335394P.
03-DEC-2001; 2001US-0335394P.
14-DEC-2001; 2001US-034393P.
06-JAN-2002; 2002US-034721IP.
10-JAN-2002; 2002US-034731IP.
13-FEB-2002; 2002US-0355250P.
13-FEB-2002; 2002US-035800P.
29-MAR-2002; 2002US-0368809P.
04-APR-2002; 2002US-0368809P.
                                                                                                                                                                                                                                                                                                                 (EOSB-) EOS BIOTECHNOLOGY INC
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22-JUL-2002; 2002US-0397845P.
09-SEP-2002; 2002US-0409450P.
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05-JUN-2002; 2002US-0386614P
16-JUL-2002; 2002US-0396839P.
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Murray R,
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P-PSDB; ADN39628.
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Hevezi PA; A;

Gish KC, Glynne R, Wilson KE, Zlotnik

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The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
other diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
patient by detecting a nucleic acid at least 80% identical to those of
the invention or by detecting a polypeptide of the invention. The
invention also relates to expression vectors and host cells comprising a
nucleic acid of the invention; antibodies which specifically bind a
polypeptide of the invention; use of such antibodies for drug targeting;
and methods of screening for modulators of activity or expression of the
polypeptides and nucleic acids. The nucleic acids, polypeptides,
antibodies and methods are useful for diagnosing, prognosing and treating
cancer and other conditions such as psoriasis; ischaemia, heart disease,
altherosclerosis, inflammatory diseases, autoimmune diseases, retinal
neovascularistation syndromes, scarring and uterine fibroids. They may
also be useful in wound healing and in contraception. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence represents a nucleic acid sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3032 BP; 729 A; 816 C; 648 G; 839 T; 0 U; 0 Other;
Claim 8; SEQ ID NO A227; 1385pp; English.
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ADN39627

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13-NOV-2002; 2002WO-US036810.

22-MAY-2003

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The invention relates to nucleic acids and proteins (ADN)8683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
cuber diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
patient by detecting a nucleic acid at least 80% identical to those of
the invention or by detecting a polypeptide of the invention. The
invention also relates to expression vectors and host cells comprising a
nucleic acid of the invention; antibodies which specifically bind a
polypeptide of the invention; use of such antibodies for drug targeting;
and methods of screening for modulators of acitivity or expression of the
polypeptides and nucleic acids. The nucleic acids, polypeptides,
antibodies and methods are useful for diagnosing, prognosing and treating
cancer and other conditions such as psoriasis, ischaemia, heart disease,
atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
neovascularistation syndromes, scarring and uterine fibroids. They may
also be useful in wound healing and in contraception. The present
                                                                                      Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence represents a nucleic acid sequence of the invention.
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                                                                                                                                                                               Claim 8; SEQ ID NO A130; 1385pp; English
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Matches 2724; Conservative
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                             CCTCCCAGTTCCGTGCCATCACCAGCTTATCCAGTGACTGAGAGCTGCCATCTTTCCTCT
                                                            ATCTTGTTCAATCCTCACTTTAAGGAGGATCTGGTGAGCCTGAGAAAGCAAACCTACGTC
                                                                                             2661 ATCTTGTTCAATCCTCACTTTAAGGAGGATCTGGTGAGCCTGAGAAAGCAAACCTACGTC
                                                                                                                                                   TGGACAAGATCAAAACACCCCAAGCTTGATGTCAATTAACTCTGATGATGTCGAAAAACAG
                                                                                                                                                                                             2721 regacaagarcaaaacacccaagcrigarcraarraacrcreargargricgaaaaacag
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Wilson KE, Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; differential expression; cancer; angiogenic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                            GTGGCATTTGTCCCATGTCTCTAA 2724
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Murray R, Watson SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADN39530 standard; cDNA; 3032
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2001US-0332464P.
2001US-0334393P.
2001US-0335394P.
2001US-0340376P.
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2002US-0347349P.
2002US-0355250P.
2002US-0356714P.
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2002US-0368809P.
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2002US-0397775P.
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03-DEC-2001;
14-DEC-2001;
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10-JAN-2002;
08-FEB-2002;
13-FEB-2002;
20-FEB-2002;
29-MAR-2002;
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The invention relates to a combination comprising cDNAs that are differentially expressed in response to steroid treatment. Also included are the following: a high throughput method for using a cDNA to detect differential expression of nucleic acids in a sample; and a high throughput method of screening molecules or compounds to identify a ligand that specifically binds a cDNA. The sample is from a subject with Wilson disease and comparison of a standard defines a stage of that disease. The high throughput method of screening molecules or compounds to identify a ligand that specifically binds a cDNA comprises; combining the combination with molecules or compounds under conditions to allow specific binding; and detecting specific binding between each cDNA and at least one molecule or compound. The molecules or compounds are regulatory proteins. The combination is useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis or hepatitis. The present sequence represents a human cDNA which is differentially expressed in steroid-induced CSA liver cells. Note: The sequence data for this parent did not form part of the printed sequence data sequence data for this parent did not form part of the printed sequence data sequence data for this parent did not form part of the printed sequence data sequence data for this parent did not form part of the printed sequence data sequence data for this parent did not form part of the printed sequence data sequence data of the printed sequence data sequence data of the printed sequence data sequence data of the data for this parent did not form part of the printed sequence data sequence data of the data for this parent did not form part of the printed sequence data sequence data of the data for this parent did not form part of the printed sequence data sequence data of the data for this parent did not form part of the data for t
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Deery Match 100.04; Score 2724; DB 12; Length 4570; Beet Local Similarity 100.04; Pred. No. 0; 1

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This invention relates to a novel method of identifying ligands to an orphan receptor protein which comprises transforming cells with DNA encoding a fusion protein of the orphan receptor with a fluorescent protein, so that the fusion protein is expressed in the cells (or cell membranes isolated from them) and contacting the cells with the potential ligand to be tested. A suitable fluorescent protein for incorporation in the fusion protein is green fluorescent protein (GFP), for example GFP-1, wild-type GFP, GFPUV or Enhanced GFP (EGFP). The method is useful for the identification of ligands binding to an orphan receptor protein.
                                                                            Transformation of cells with a fusion protein of an orphan receptor protein with a fluorescent protein useful for identification of ligands to the orphan receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-CAA940967) and AAY90683-Y90681), and to DNA encoding them (AAA30709-A30743 and AAA30775-A3079). The mutant proteins of the invention contain a contain a mattion in a portion of the protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acid No.-terminal of an endogenous prolline in TM6 to form a sequence X-CC (AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Pro may be endogenous, non-endogenous, or a mixture of endogenous and non-endogenous cresidues. The constitutively active GPCRs are useful for identifying antagonists and partial agonists for use as pharmaceutical celucidating the roles of the receptors in normal and diseases and disorders associated with that receptors in normal and diseases and disorders associated with that receptors in normal and diseases and disorders associated with that receptors. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous ligands. Sequences AAA30709-
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        encoding human mutant G protein-coupled receptor HG38 (V765K)
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Pred. No. 0;
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                                                protein-coupled receptor; GPCR; constitutively active;
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Matches 2722; Conservative
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Sequence 263. Application US/09170496D

Sequence 263. Application US/09170496D

Patent No. 6555339

GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Law, Chen W.
TITLE OF INVENTION: No. 655539-Endogenous, Constitutively Activated Human G Protein TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040

CURRENT APPLICATION NUMBER: US/09/170,496D

CURRENT FILING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 294

SOFTWARE PATENTIN Version 3.1

SEQ ID NO 263

LENGTH: 2724
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ative 0; Mismatches
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Best Local Similarity 100.
Matches 2724; Conservative
  , ORGANISM: Homo sapiens
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    RESULT 1
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Sequence 220, App
Sequence 260, App
Sequence 5, Appli
Sequence 669, Appli
Sequence 669, Appli
Sequence 4412, App
Sequence 12411, App
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Sequence 139111,
Sequence 2145, Ap
Sequence 4695, Ap
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12140, A
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Sequence 17248, A
Sequence 13818, A
                                                                                          July 12, 2005, 20:35:13; Search time 447 Seconds (without alignments) 9971.404 Million cell updates/sec
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Sequence 134705,
Sequence 153352,
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Sequence 277, P
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-266-225b-9
US-09-249-016-6412
US-09-949-016-1211
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Patent No. 655339
GENERAL INPORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Con;
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 277
LENGTH: 2724
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Pred. No. 0;
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US-09-170-496D-261

Sequence 261, Application US/09170496D

Sequence 261, Application US/09170496D

Sequence 261, Application US/09170496D

Sequence 261, Application US/09170496D

GRNERAL INFORMATION:

APPLICANT: Chalmers, Derek T.

APPLICANT: Liaw, Chen W.

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
TITLE OF INVENTION: No. 6555339-Endogenous, CONSTITUTION OF INVENTION: Receptors

TITLE OF INVENTION: NOW NUMBER: US/09/170, 496D

CURRENT FILING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 294

SEQ ID NO 261

LENGTH: 25
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Sequence 260, Application US/09170496D

Patent No. 655539

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Receptors
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT PAPLICATION NUMBER: US/09/170,496D
CURRENT PILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
SEQ ID NO 260
LENGTH: 30
601 GCTCTATGGTAAAACACATTGCCCTGTTGCTCTTCACCAACTGCATCCTAAACTGCCCTG 660
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100.0%; Pred. No. 0.021;
tive 0; Mismatches (
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Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 24; Conservative 0; Mismatches
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US-09-170-496D-260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: No. 6555339el Sequence
US-09-170-496D-261
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ORGANISM: Artificial Sequence
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US-09-170-496D-260/c
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                                                                 Sequence 220. Application US/09495050A
| Sequence 220. Application US/09495050A
| Patent NO. 6492505
| GENERAL INFORMATION:
| APPLICANT: Roopa', Reddy
| APPLICANT: Roopa', Marice
| TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED FITLE OF FILLS PAPLICATION NUMBER: US/09/495,050A
| CURRENT FILLING DATE: 2000-01-31
| PRIOR FILLING DATE: February 1, 1999
| NUMBER OF SEQ ID NOS: 305
| SOFTWARE: PERL PROGram
| SEQ ID NO 220
| LENGTH: 723
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; OTHER INFORMATION: Incyte ID No. 6492505 2603450CT1
US-09-495-050A-220
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ORGANISM: Homo sapiens
                                            RESULT 4
US-09-495-050A-220
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igaquence 4412, Application US/09949016
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igaquence 4412, Application US/09949016
igaquence 4412, Application US/0949016
igansAL INFORMATION:
i APPLICANT: VENTER, J. Craig et al.
i TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
i TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
i CURRENT APPLICATION NUMBER: US/09/949,016
i CURRENT FILING DATE: 2000-04-14
i PRIOR APPLICATION NUMBER: 60/231,768
i PRIOR FILING DATE: 2000-10-20
i PRIOR FILING DATE: 2000-10-03
i PRIOR FILING DATE: 2000-09-08
i NUMBER OF SEQ ID NOS: 207012
i SOFTWARE: FastSEQ for Windows Version 4.0
i SEQ ID NO 4412
i LENGTH: 2910
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                                                                                           Length 2896;
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                                                                                                                                      0; Indels
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                                                                                           DB 4;
3.6;
                                                                                        Query Match 0.8%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 3.6 Matches 21; Conservative 0; Mismatches
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Best Local Similarity 100.0
Matches 21; Conservative
  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-266-225D-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Human
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US-09-949-016-4412
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LENGTH: 2906
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                                                           APPLICANT: Pulet, Stefan M.
APPLICANT: Scoles, Daniel R.
TITLE OF INVENTION: UNCLEIC ACID ENCODING
TITLE OF INVENTION: SCHWANNOMIN-BINDING-PROTEINS AND PRODUCTS RELATED THERETO
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES, LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
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Sequence 9, Application US/09266225D

Patent No. 6573364

GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishan
APPLICANT: Kingsmore, Stephen
APPLICANT: Tchernev, Velizar
TITLE OF INVENTION: Syndrome (HPS) Protein Complexes and HPS Protein
TITLE OF INVENTION: Syndrome (HPS) Protein
TITLE OF INVENTION: Interacting Proteins
FILE REFERENCE: 15966-523
CURRENT APPLICATION NUMBER: US/09/266,225D
CURRENT PILING DATE: 1999-03-10
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                          ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,089
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 60/030,987
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ramos, Robert T.
REGISTRATION NUMBER: 37,915
REFERENCE/DOCKET NUMBER: 9P-CE 2862
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
TELEPHONE: (619)535-9001
TELEPHONE: (619)535-9001
TELEPHONE: (619)535-901
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Sequence 5, Application US/08971089
Patent No. 6376174
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Best Local Similarity 100.(
Matches 21; Conservative
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US-08-971-089-5
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Gaps

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Sequence 17449, Application US/09949016
; Sequence 17449, Application US/09949016
; Batent No. 6812339
; GENERAL INFORMATION:
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    FILE OF INVENTION NUMBER: US/09/949,016
; CURRENT APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR PILING DATE: 2000-10-20
; PRIOR PILING DATE: 2000-10-20
; PRIOR PILING DATE: 2000-10-20
; PRIOR PILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SEQ ID NOS: 207012
; SEQ ID NO 1248
                                                            Length 22339;
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; Patent No. 663963
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; TITLE REFERENCE: GENSET. 054PR.
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
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Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 21; Conservative 0; Mismatches
                                                         0.8%; Score 21; DB 4;
100.0%; Pred. No. 4.2;
                                                                                ilarity 100.0%; Pred. No. 4.7
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (1)...(61198); OTHER INFORMATION: n = A,T,C or GUS-09-949-016-17248
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; OTHER INFORMATION: n=a, g, C
US-09-621-976-13818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
                                                                                Local Similarity
nes 21; Conserv
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               US-09-949-016-16154
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                                                              Query Match
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Matches
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US-09-949-016-16154

Sequence 16154, Application US/09949016

Sequence 16154, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMOKENISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPRENSICE: CLOL01307

CURRENT APPLICATION NUMBER: US/99/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PAPLICATION NUMBER: 60/237,768

PRIOR PELING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 16154

LENGTH: 22339
                                                                                                                                                                                                                                                Sequence 12411, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 08/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0
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0.8%; Score 21; DB 4; Length 22339;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 21; Conservative 0; Mismatches 0; Indels
                                     Indels
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                 Pred. No. 3.6; Mismatches
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                                                                                     2159 CCAGCACCATGGGCTACATGG 2179
                                                                                                                   2151 CCAGCACCATGGCTACATGG 2171
100.0%; Pre-
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12411
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NAME/KEY: misc_feature
LOCATION: (1)...(22339)
OTHER INFORMATION: n = A,T,C or G
                 Best Local Similarity 100.
Matches 21; Conservative
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US-09-949-016-12411
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LENGTH: 22339
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Sequence 14190, Application US/09270767

Sequence 14190, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270, 767

CURRENT PILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 14190

LENGTH: 574
                                                     Gaps
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Query Match 0.7%; Score 20; DB 4; Length 443; Best Local Similarity 100.0%; Pred. No. 11; Matches 20; Conservative 0; Mismatches 0; Indels
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0.7%; Score 20; DB 4; Length 574;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                              255 CCTGCCCAGTCTCGCTTCC 274
315 CCTGCCCAGTCTCGCTTCC 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    715 TTAGATTTAAATTACAATAA 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA; ORGANISM: Drosophila melanogaster
US-09-270-767-14190
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Search completed: July 13, 2005, 03:13:17 Job time : 457 secs

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July 12, 2005, 21:05:53; Search time 1607 Seconds (without alignments) 10642.288 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                          6330945 seqs, 3139162390 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Listing first 45 summaries
                                                                                   OM nucleic - nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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ptodata/2/pubpna/US10H_PUBCOMB.seq:* ptodata/2/pubpna/US10I_PUBCOMB.seq:* ptodata/2/pubpna/US10 NEW PUB.seq:* prodata/2/pubpna/US10E_PUBCOMB.seq:* prodata/2/pubpna/US10F_PUBCOMB.seq:* ptodata/2/pubpna/US10G_PUBCOMB.seg: ptodata/2/pubpna/US10A_PUECOMB.seq: ptodata/2/pubpna/US10B_PUBCOMB.seq: ptodata/2/pubpna/US10C_PUBCOMB.seq: ptodata/2/pubpna/US10D_PUBCOMB.seq: prodata/2/pubpna/US09A_PUBCOMB.seq: prodata/2/pubpna/US09B_PUBCOMB.seq: prodata/2/pubpna/US09C_PUBCOMB.seq: prodata/2/pubpna/US09C_PUBCOMB.seq: prodata/2/pubpna/US09_NEW_PUB.seq: /2/pubpna/US11A PUBCOMB.seq PUBCOMB.seq:* /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq: pubpna/USO7_NEW_PUB.seq: /pubpna/PCTUS_PUBCOMB.seq: /pubpna/USO8_NEW_PUB.seq: /pubpna/USO8_PUBCOMB.seq: ptodata/2/pubpna/PCT ptodata/2/ ptodata/2, ptodata/2, /cgn2_6/F /cgn2_6/P 19: 20:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Sequence 263, App	Sequence 421, App	Sequence 4, Appli	Sequence 21, Appl	Sequence 1114, Ap	Sequence 157, App	Sequence 48, Appl
SUMMARIES	1		US-10-251-385-263		US-10-174-456-4	US-10-751-736-21	US-10-295-027-1114	US-10-482-029-157	US-10-651-237-48
	Query Match Length DR ID	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2724 15						
de		•	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score		2724	2724	2724	2724	2724	2724	2724
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Sequence 48, Appl Sequence 945, Appl Sequence 205, Appl Sequence 277, Appl Sequence 113, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 2009, Appl Sequence 2009, Appl Sequence 2009, Appl Sequence 2009, Appl Sequence 20935, Sequence 299355, Sequence 2050, Appl	314112 314112 314115 314115 7, App 11,	
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ALIGNMENTS

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Sequence 263, Application US/10251385
Publication No. US20030105292A1
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Protein-Coupled
FILE REPERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
CORRENT FILING DATE: 1998-10-13
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2724; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 294
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EXPRESSION

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ATCTTGTTCAATCCTCACTTTAAGGAGGATCTGGTGAGCCTGAGAAAGCAAACCTACGTC 2520	CCTCCCAGTTCCGTGCCATCACCAGCTTATCCAGTGACTGAGAGCTGCCATCTTTCCTCT 2700	GTGGCATTTGTCCCATGTCTCTAA 2724 		; Sequence 21, Application US/10751736 ; Publication No. US20040265230A1 ; RENERAL INFORMATION: ; APPLICANT: Wyeth	Martinez, Robert Brown, Eugene Liu, Wei FENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON	TITLE OF INVENTION: CANCERS FILE REFERENCE: AM100927 (031896-002000) CURRENT APPLICATION NUMBER: US/10/751,736 CURRENT FILING DATE: 2003-01-06	*ATION NUMBER: US Provisional Application 60/438,000 ; DATE: 2003-01-06 ; DA NOS: 54873 :tentIn version 3.2	; SEQ ID NO 21 ; LENGTH: 2724 ; TYPE: DNA ; ORGANISM: Homo sapiens	:-10-751-736-21 Query Match Best Local Similarity 100.0%; Score 2724; DB 20; Length 2724; Best Local Similarity 100.0%; Pred. No. 0; O. 100.0; O. Indels 0; Gabs 0;	recegerrestrate record control of the control of th			CCTTCCAACCTCAGGGTCTTCACCTACCTAGGGTATGAACAACATCAGTCAG	CTGCTCCCGAATCCCCTGCCCAGTCTCCGCTTCCTGGAGGTTACGTCTTGCGGGAAC 300 	GCTCTGACATACATTCCCAAGGGAGCATTCACTGGCCTTTACAGTCTTAAAGTTCTTATG 360

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US-10-782-413-48

Sequence 48, Application US/10782413

Publication No. US20050048526A1

GENERAL INFORMATION:

APPLICANT: Ortho-Clinical Diagnostics, Inc.

APPLICANT: Wangy, Yixin

TILE OP INVENTION: COLORECTAL CANCER Prognostics

FILE REFERENCE: VDX-5002 CIP

CURRENT APPLICATION NUMBER: US/10/782,413

CURRENT PILING DATE: 2004-02-18

PRIOR PILING DATE: 2003-08-28

NUMBER OF SEQ ID NOS: 94

SOFTWARE: PALENTIN VERSION 3.1

SEQ ID NO 48

LENGTH: 2880

TYPE: DATE: DATE: CANCER DATE: CANC
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2724; Conservative 0; Mismatches
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APPLICANT: A CAIR.

APPLICANT: A CAIR.

APPLICANT: A CAIR.

APPLICANT: Glanberg, Wendy M.

APPLICANT: Glanberg, Wendy M.

APPLICANT: Glanberg, Wendy M.

APPLICANT: Glanberg, Wendy M.

APPLICANT: Glanberg, Packer A.

APPLICANT: Mateon, Sugan R.

APPLICANT: MATEON REPLICANTON NUMBER: US 6063,733

PRIOR APPLICANTON NUMBER: US 60/330,666

PRIOR APPLICANTON NUMBER: US 60/330,666

PRIOR PRILING DATE: 2001-11-13

PRIOR PLILING DATE: 2001-11-12

PRIOR PLILING DATE: 2001-11-21

PRIOR APPLICANTON NUMBER: US 60/334,339

PRIOR PLILING DATE: 2001-11-21

PRIOR APPLICANTON NUMBER: US 60/340,316

PRIOR APPLICANTON NUMBER: US 60/355,250

PRIOR APPLICANTON NUMBER: US 60/355,250

PRIOR PRILING DATE: 2002-01-10

PRIOR PLILING DATE: 2002-02-03

PRIOR PLILING DATE: 2002-02-13

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k; Pred. No. 0;
0; Mismatches
  2749 GTGGCATTTGTCCCATGTCTCTAA 2772
                                                                                                                              ; Sequence 848, Application US/10295027; Publication No. US20030232350A1; GENERAL INFORMATION:
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100.0%;
Best Local Similarity 100.0%;
Matches 2724; Conservative 0
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US-10-295-027-848
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Matches 2724; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 ATGGACACCTCCGGGTGTGCTCTGCTGTGCTGTGCTGCTGCTGCTGC	QY 301 GCTCTGACATACATTCCCAAGGGACATTCACTGGCCTTTACAGTCTTATG 360 Db 501 GCTCTGACATACATTCCCAAGGGACATTCACTGGCCTTTACAGTCTTAAAGTTCTTATG 560 QY 361 CTGCAGAATAATCAGCTAAGACACTCACCACAGAAGTCTTGCAAGCCTT 420 Db 561 CTGCAGAATAATCAGCTAAAGACACTCACCACAGAAGTTTGCAAAGCTT 620 QY 421 CAATCCCTGGGTCTGAAGACCACATCAGCTATGTGCCCCCAAGATTTGCAAAGCTT 620 Db 621 CAATCCCTGGGTCTGAATGTTACTGCCCCCAAGCTGTTTCAGTGGC 680 QY 481 CTGCATCTGAGTCTGGATGCTAACACTATGTGCCCCCCAAGCTGTTTCAGTGGC 680 QY 481 CTGCATTCCCTGAGTGCTGATGCTAACACTATGTGCCCCCAAGTGTTTCAGTGGC 690 QY 481 CTGCATTCCCTGAGGCACCTGGATGGATGACACATACGGTTAACAGAAATCCCCGTCCAG 540 Db 621 CTGCATTCCCTGAGGCACCTGGATGACAATGCGTTAACAGAAATCCCCGTCCAG 540 Bb 621 CTGCATTCCCTGAGGCACCTGGATGACAATGCGTTAACAGAAATCCCCGTCCAG 540 CTGCATTCCCTGAGGCACCTGGGATGACAATGCGTTAACAGAAATCCCCGTCCAG 540	0y 541 GCTTTTAGAAGTTTATCGGCATTGCAAGCATTGGCCCTGAACAAATACACCAC 600 Db 741 GCTTTTAGAAGTTTATCGGCATTGCAAGCATGGCCTTGGCCTTGAACAAATACACCAC 800 Qy 601 ATACCAGACTATGGAAACCTCTCCCAGCTTGGTAGTTCTACATCTCCATAACAAT 660 Db 801 ATACCAGACTATGGAAACCTCTCCCAGCTTGGTAGTTCTACATCTCCATAACAAT 860 Qy 661 AAACCAGTCCTGGGAAACAAATGCTTTGGTAGTTCTACATCTCCATAACAAT 860 Db 861 AGAATCCACTCCTGGGAAACAAATGCTTTGATGGGCTCCACAGCCTAGAGACTTTAGAT 720 Qy 721 TTAAATTACAATAACAATAACATTGATGGGCTCCACAGCCTTAAA 780 Db 921 TTAAATTACAATAACATAACATTGAATTCCCCACTGCAATTAGGACCTCTCCAACCTTAAA 980	
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jeublicant: Atar, Daniel
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Matches 1864; Conservative 0; Mismatches
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APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
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APPLICANT: Matson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Gos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REPERRECE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT APLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2000-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-11-20
PRIOR PLING DATE: 2001-11-3
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1864; Conservative 0; Mismatches 0;
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; ORGANISM: Homo sapiens
US-10-295-027-1113
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	AGCTCTACTGCAATTTGGACAAGGGGACCTGGAGAATATTTGGGACTGCTCTATGGTAA 	2297 AACACATTGCCCTGTTGCTCTTCACCAACTGCATCCTAAACTGCCCTGTGGCTTTCTTGT 2356 	2357 CCTTCTCCTCTTTAATAAACCTTACATTTATCAGTCCTGAAGTAATTAAGTTTATCCTTC 2416 	2417 TGGTGGTAGTCCCACTTCCTGCATGTCTCAATCCCCTTCTCTACATCTTGTATAATCCTC 2476	2477 ACTTTAAGGAGATCTGGTGAGCCTGAGAAAGCAAACCTACGTCTGGACAAAGAAAAC 2536 	2537 ACCCAAGCTTGATGTCAATTAACTCTGATGATGTCGAAAAACAGTCCTGTGACTC 2596 	2597 AAGCCTTGGTAACCTTTACCAGCTCCAGGATCACTTATGACCTGCCTCCCAGTTCCGTGC 2656 2525 AAGCCTTGGTAACCTTTACCAGCTCCAGGATCACTTATGACCTGCCTCCCAGTTCCGTGC 2584	2657 CATCACCAGCTTATCCAGTGACTGAGAGCTGCCATCTTTCCTCTGTGGCATTTGTCCCAT 2716	2717 GTCT 2720 2645 GTCT 2648
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. OM nucleic - protein search, using frame_plus_n2p model Run on: July 13, 2005, 03:05:50; Search time 50.5 Seconds (without alignments) 10379.979 Million cell updates/sec 1077 Perfect score: 907 Scoring table: US-10-751-736-21 Scoring table: OLIGO Kgapop 60.0, Kgapext 60.0 Kgapop 60.0, Ygapext 60.0 Kgapop 60.0, Ygapext 60.0 Kgapop 60.0, Pgapext 7.0 Searched: 283416 seqs, 96216763 residues Word size: 1 Total number of hits satisfying chosen parameters: 565918 Minimum DB seq length: 2000000000 Post-processing: Listing first 45 summaries	Command line parameters:

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conserved hypothetical protein Atu0506 [imported] - Agrobacterium tumefaciens (strain CS C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Saccession: AF2638
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2333, 2001
A; Atthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                        ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.

A;Accession: AP2638

A;Status: preliminary

A;Status: preliminary

A;Molecule type: DNA

A;Cross-references: UNIPROT:Q8UHZ5; GB:AE008688; PIDN:AAL41524.1; PID:g17738854; GSPDB:G-C;Genetics: A;Gene: Aru0506

A;Experimental source: strain CS8 (Dupont)

A;Genetics

A;Gene: Atu0506

A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q8UHZ5; GB:AE007869; PIDN:AAK86320.1; PID:g15155438; GSPDB:G
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Grotein-coupled receptor FEX - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C;Accession: JG0193
R;Hermey, G.; Methner, A.; Schaller, H.C.; Hermans-Borgmeyer, I.
R;Hermey, G.; Methner, A.; Schaller, H.C.; Hermans-Borgmeyer, I.
A;Accession: JG0193
A;Title: Identification of a novel seven-transmembrane receptor with homology to A;Reference number: JG0193; MUID:9912127; PMID:9920770
A;Accession: JG0193
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-907 <HER>
                                                                                                    2400
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                                                                SerCysAspSerThrGlnAlaLeuValThrPheThrSerSerIleThrTyrAspLeu 880
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                                                                                                    CCTGTGGCTTTCTTGTCCTTCTCTCTTTAATAAACCTTACATTTATCAGTCCTGAAGTA
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C;Accession: A71400
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirks, Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Gielf avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B. Nature 391, 485-488, 1998
A;Authors Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech, erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ansk Ajritle: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal) A;Accession: A71400; MUID:98121113; PMID:9461215
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A;Cross-references: UNIPROT:P73551; EMBL:D90907; GB:AB001339; NID:g1652618; PIDN:BAA17591
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cjaccession: 577257
Rjacession: 577257
Rjaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Rjaneko, T.; Sato, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                   A; Cross-references: UNIPROT: 023253; GB: Z97335; NID: 92244747; PID: e326857; PID: 92244748
C; Genetics:
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C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 08-Oct-1999
C;Accession: S07957
R;Plasterk, R.H.A.; van de Putte, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein s111265 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
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A; Status: nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
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                                                                                                                                                              with ted to the EMBL Data Library, October 1996
A;Reference number: 219578
A;Accession: T25341
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residus: preliminary;
A;Residus: 1-342 < WILD-
A;Cross-references: UNIPROF. Q9XVN1; EMBL: Z81086; PIDN: CAB03117.1; GSPDB: GN00019; CESP:FS
A;Experimental source: clone F5386
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probable disease resistance protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
                                                  hypothetical protein F53B6.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;baceis: Caenorhabditis elegans
C;bace: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22541
R;White, S.
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A,Genetic code: SGC3
C,Keywords: mitochondrion
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A;Gene: CESP:F53B6.4
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okat, G.; Madueno, E.; Maitournam, A.; Ma
Vazquez-Boland, J.A.; Voss, H.; Wehland,
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A;Wolecule type: DNA
A;Residues: 1-150 «GLA>
A;Cross-references: UNIRROT:092BJ1; GB:AL592022; PIDN:CAC96788.1; PID:gl6414044; GSPDB:G
A;Experimental source: strain Clip11262
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A;Cross-references: UNIPROT:016345; EMBL:AF016436; PIDN:AAC25897.1; GSPDB:GN00023; CESP:
A;Experimental source: strain Bristol N2; clone F38H12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F38H12.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31777
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   Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-i A;Titerec, Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1627
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A;Description: The sequence of C. elegans cosmid F38H12.
A;Reference number: Z21084
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N;Molecule type: DNA
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A,Introns: 27/1; 38/3; 107/3
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Pred. No.:
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Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
Cipacesion: AB1265
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A; Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUD:21537279; PMID:11679669
A;Accession: AB1265
A;Anleutery Ap1265
A;Anleutery Ap1265
A;Anleuter pre-1074
A;Anleuter pre
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD1627
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
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A;Cross-references: UNIPROT:Q93RD9; GB:NC_003210; PIDN:CAC99600.1; PID:g16410951; GSPDB:
A;Experimental source: strain EGD-e
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AD1627
hypothetical protein homolog lin1557 [imported] - Listeria innocua (strain Clip11262)
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hypothetical protein lmo1522 [imported] - Listeria monocytogenes (strain EGD-e)
EMBO J. 4, 237-242, 1985

A;Title: The invertible P-DNA segment in the chromosome of Escherichia coli.
A;Reference number: S07185; MUID:85257443; PMID:3894006
A;Accession: S07957
A;Accession: S07957
A;Status: translation not shown
A;Nolecule type: DNA
A;Residues: 1-145 < PLA>
A;Residues: 1-145 < PLA>
A;Residues: 1-15 < PLA>
A;Residues: 1-15
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C;Superfamily: conserved hypothetical protein H10670
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A87605
Dps family protein [imported] - Caulobacter crescentus
C;Species Caulobacter crescentus
C;Species Caulobacter crescentus
C;Species Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: A87605
R;Nicerman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad Sci. U.S.A. 98, 4136-4441, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87509
A;Reference number: A87605
A;Scatus: preliminary
A;Molecule type: DNA
A;Residues: 1-178 <STO>
A;Crossion: A87605
A;Crossion: A87605
A;Genetics: C;Genetics: UNIPROT:Q9A4G1; GB:AE005673; NID:g13424489; PIDN:AAK24837.1; GSPDB:CC;Genetics:
A;Gene: CC2873
A,Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A,Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: F97440
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-162 <KUR>
                                                                                                                                                        A;Cross-references: UNIPROT:Q8U518; GB:AE007869; PIDN:AAK86479.1; PID:g15155627; GSPDB:q
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Whypotherical protein c05017 - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 11-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Date: 11-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Date: 11-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S Mol. Microbiol. 22, 175-191, 1996
Mol. Microbiol. 22, 175-191, 1996
A;Title: Organizational characteristics and information content of an archaeal genome: A;Feference number: S73076; MUID:97055432; PMID:8899719
A;Accession: S75434
A;Resion: S75434
A;Resion: Lucye: DWA
A;Residues: 1-179 <SEN>
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A,Map position: circular chromosome
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A;Cross-references: UNIPROT:P96006; EMBL:Y08257; NID:g170772; PID:e283869; PID:g1707840
A;Experimental source: strain P2
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996
C;Genetics:
A;Start codon: GTG
Alignment Scores:
Pred: No.:
Score:
B: 00.00*
Matches:
Pred: No.:
Conservative: 0
Best Local Similarity: 100.00*
Rimmatches: 0
Best Local Similarity: 100.00*
Rimmatches: 0
Duery Match: 2
Best Local Similarity: 100.00*
Us-10-751-736-21 (1-2724) x S75434 (1-179)
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Search completed: July 13, 2005, 03:58:32 Job time: 83.5 secs

2035 TCTAGCCTGAAAGTAATCATTTTG 2058

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Run on:

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CD617343 550130501
CD617351 55013056J
CD617359 55013056J
CD617359 55041471J
AQ076504 CIT-HSP-2
CD617344 55013051H
CD617354 550414150
AIS99105 tp78b01.x
AIS99105 tp78b01.x
AIS92439 Wq52c12.x
AINJ9316 WRO-GN002
CC6333257 AGENCOURT
CD617345 55013051J
BS7762 CIT-HSP-201
AISC192 qT22d02.x
CE133614 tigr-268-x
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1 (bases 1 to 2724)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Rerriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, White, T.J., Sninsky, J.J.,
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Direct Submitseion
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Homo sapiens GPR49 gene, VIRTUAL TRANSCRIPT, partial sequence,
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100.0%; Pred. No. 0;
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CD61757
CD617358
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CD617359
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AD61
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/db_xref="taxon:9606"
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CF177761
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/locus_tag="HCM4322"
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Homo sapiens
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- 2005 Compugen Ltd.
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AA460529
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                        GenCore
Copyright (c) 1993
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seq length: 200000000
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1569 MAINTECTGGTTGACTTTGACATTGCACGTGAAAGCCTTCATTCAGTGCAGTGTGACTTCACCTGCAGGTGTGAATTGC 1638 1629 PICCCCCAGGCCCTTCAAACCCTTCAAACCCTTCAATTGCTTCAGTGCAAATTGC 1638 1629 PICCCCCCAGGCCCTTCAACCCTTCATCATCAGTGCAGTTCAAATTGC 1638 1639 ATGCCCCTTCAACCCTTCAACCCTTCATCATCAGTGCAGTTCAACTTCAACCTTCAACCTTCAACCTTCAACTTCAACCTTCA
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429 GCGTCTGGATGCTGACCACATCACTATGCTCACACCTGATACACACTCCTCACGCTTTTTTC 548 449 CCTGAGGCACTGTGGATGCACACACACTCACACACACTCCACACACTCCACACACA

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RSTI5934 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
BG196708.1 GI:13718395
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 800)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
Mhittington,J., Lerner,L., Costanaco,D., McBligott,K., Boozer,S.,
Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
Offenbacher,J., Danzig,J. and Ducar,M.
Creation of gene expression
activation of gene expression
                                                                                                                                                                                         1103 CCAGTTTTTCAGTCTGCCAAAAGCTTCAGAAATTGACCTAAGACATAATGAAATCTACG 1162
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                                                                              301 CAAACCTGGAGAGTCTGACTTTAACTGGAGCACAGATCTCATCTTCCTCAAACCGCCT
                                                                                                                           GCAATCAGTTACCTAATCTCCAAGTGCTAGATCTGTCTTACAACCTATTAGAAGATTTAC
                                                                                                                                           361 GCAATCAGTTACCTAATCTCCAAGTGCTAGATCTGTCTTACAACCTATTAGAAGATTTAC
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                                                                                                                                                                                                                                                                      541 ACAAAATTGCTATTATTCACCCCCAATGCATTTTCCACTTTGCCATCCCTAATAAAGCTGG
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   GAACACTGACTCTGAATGGTGCCTCACAAATAACTGAATTTCCTGATTTAACTGGAACTG
                                                              CAAACCTGGAGAGTCTGACTTTAACTGGAGCACAGATCTCATCTTCCTCAAACCGTCT
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Nat. Biotechnol. 19 (5), 440-445 (2001)
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                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/organism="Homo sapiens"
/db xref="taxon:960"
/db xref="taxon:960"
/clone="CSODE007YC19"
/tissue type="PLACENTR"
/clone_lib="Homo sapiens PLACENTR"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and SCRV sites of the pCMVSPORT 6 vector. Library was not normalized."
                                                                                                                                                                     AL541959 1060 bp mRNA linear EST 24-MAR-2004 AL541959 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE007YC19 5-FRIMS, mRNA sequence.
AL541959.3 GI:45717535
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AATTCCCCACTGCAATTAGGACACTCTCCAACCTTAAAGAACTAGGATTTCATAGCAACA
ATATCAGGTCGATACCTGAGAAAGCATTTGTAGGCAACCCTTCTCTTATTACAATACATT
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951; Conservative 0; Mismatches
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1 (Bases to 1104)

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1 (Bases to 1104)

2 (Stuber, C., Jessee, J. and Polayes, D.

1 (Dupublished (2001)

2 (Dupublished (2001)

3 (2001 this sequence version replaced gi:31068631.

3 (Contact: Genoscope (2001)

4 (Contact: Genoscope (2002)

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                             1104 bp mRNA linear BST 24-MAR-200·
AL530798 Homo sapiens NEUROBLASTOWA COT 50-NORMALIZED Homo sapiens
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/db xref="taxon:9606"
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/coll_line="HT1080"
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/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression,
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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Location/Qualifiers
   Cleveland,
3201 Carnegie Ave, Clevela
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E. I. (Bases 1 to 671)

S. Kim, N. S., Hahn, Y., Oh, J. H., Lee, J. Y., Ahn, H. Y., Chu, M. Y., Kim, M. R., Oh, K. J., Cheong, J. B., Sohn, H. Y., Kim, J. M., Park, H. S., Kim, S. and Kim, Y. S.

Z. Eventier Korean EST Project 2001

Unpublished (2002)

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                                                        421 GCCTATAIGCTTACCAGGGCTGIGCATTTGGAGTGTTAGAATGCCTATWAGATTTCTA
                                                                                                                                   661 ACCTGCTTGATGGCTGGTTCAGAATTGGAGTGTGGACCATAGCAGTTCTGGCACTTA
                                   GCCT-TATGCTTACCAGTGCTGTGCATTTGGAGTGTGTGAGAATGCCTATAAGATTTCTA
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S21SNU520-31-C01"
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/fissue trype="PLACENTA COT 25-NORWALIZED"
/clone_lib="Home sapiens PLACENTA COT 25-NORWALIZED"
/note="Its strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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larity 100.0%; Pred. No. 2.7e-279;
Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
                                                                                                                                                                                   BX403219.2 GI:46875014
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1 (bases 1 to 590)
Fu.G.K., Mang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput Genomics 84 (1), 205-210 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGGGAAACGCTCTGACATACATTCCCAAGGGAGCATTCACTGGCCTTTACAGTCTTAAA 351
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55041415H1 FLP Homo sapiens cDNA, mRNA sequence.
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Pred. No. 2.8e-284;
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1360 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte,com.
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100.0%; Pred. No. ...
0; Mismatches
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/db_xref="taxon:9606"
/clone_lib="FLP"
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CD617354.1 GI:40265619
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Matches 538; Conservative
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Homo saplems had acca; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. 1 (Dases 1 to 472)

E. 1 (Dases 1 to 472)

Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Morte,B., Schellenberg,K., Steptce,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. Theising,B., WashU-Merck EST Project 1997

Londact: Wilson RK Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 287 Into Minfo@image.llnl.gov) for further information.

Seq primer: -28m3 revo ET from Amersham.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 09-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                   61 CCCTCTGTACATTTCCCCCATTAAACTGTTAATTGGGGTCATCGCAGCAGTGAACATGCT
                                                                                                                                                                                                                                                           121 caceegagrerceagrecesegeregresegerecarecerreacriringecagerriec
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421 GTATGGCGCCTCCCCTCTGCCTGCCTTTTGGGGAGCCCAGCACCATG 475
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mol_type="makk"
/db_xref="GDB:604098"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dov="tryAGB:796624"
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Examinatia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Examinatia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Examinatio, Henio, Fernia, S., Newbert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.

Lumpublished (2003)

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RZPD; INAGP98N17196.

RZPD; INAGP98N17196.

RZPDILB; I.M.A.G.E. CDNA Clone Collection;

Human UnigeneSet - RZPD3 (RZPDLIB No.972)

http://www.rzpd.de/CloneCard8/Cgi-
bin/showibb pl.cgi/response7libNo=972 Contact: Ina Rolfs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BX107244 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGp998N171964 ; IMAGE:796624, mRNA sequence.
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CTGCAGAATAATCAGCTAAGACACGTACCCACAGAAGCTCTGCAGAATTTGCGAAGCCTT 557
                                                                                  CAATCCCTGCGTCTGGATGCTAACCACATCAGCTATGTGCCCCCCAAGCTGTTTCAGTGGC 480
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contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
Location/Qualifiers
                                                                                                                                        CAATCCCTGCGTCTGGATGCTAACCACATCAGCTATGTGCCCCCCAAGCTGTTTCAGTGGC
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/organism="Homo sapiens"
/mol_type="mkNA"
/db_xref="taxon:9606"
/clone="lMAGp998N171964 ; IMAGE:796624"
/dev_etage="8-9 weeks"
/lab_host="DH108"
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Tel: +55-11-2707001
Email: asimpson@ludwig.org.br
Email: saimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Gencer.
This sequence was derived from the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5&t2=IL5-CI0149-01100-224-a05&t3=2000-11-01&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 48.
Location/Qualifiers
                                                                                                                                                                                                                                                            /mol type="make" septems //mol type="make" septems //mol type="make" septems //mol type="make" septems //mol type="make" septems //mole="lorgan: colon ins; Vector: puc18; Site 1: Smal; septems //mole="Organ: colon ins; Vector: puc18; Site 1: Smal; septems //mole="Organ: colon ins; Vector: puc18; Site 1: Smal; septems //mole="Organ: colon ins; Vector: puc18; Site 1: Smal; septems //mole products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) cappilles into the pUC18 vector: Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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0; Mismatches 1;
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1 (bases 1 to 556)
10 is Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Goldman, G.H., Carvalho, A.F., Magai, M.A., Ga Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., Geoliveira, F.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                  Length 472;
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Pred. No. 7e-248;
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100.0%; Pred. No. ..
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I (Dases 1 to 2593)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Perriara, S., Wango, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, White, T.J., Shinsky, J.J.,
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                    Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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1889 ACGAAAGCTCCCTTTTCTAGCCTGAAAGTAATCATTTGCTCTGTGCCCTGCTGGCCTTG
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Pred. No. 1.8e-212;
0; Mismatches 7; Indels
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Submitted (16-NOV-2003) Celera Genomics,
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/organism="Pan troglodytes"
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/db_xref="taxon:9598"
                                                                                                                        Science 302 (5652), 1960-1963 (2003)
                                                                                                                                                                                                                                                                                                                                                                                          <1. .>2593
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/locus_tag="HCM4322"
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Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1807 Std Error: 0.00

Seg primer: -40UP from Gibco
High quality sequence stop: 307.
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/tissue_type="well-differentiated endometrial
denocarcinoma, 7 pooled tumors"
/lab host="bullos"
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/clone="Organ: ulerus, Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 374)
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2429 TCTGATGATGTCGAAAACAGTCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGC
                                                                                       2489 TCCAGCATCACTTATGACCTGCCTCCCAGTTCCGTGCCATCACCAGCTTATCCAGTGACT
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National Cancer Institute, Cancer Genome Anatomy Project
Tumor Gene Index
Unpublished (1997)
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.
Matches 369; Conservative
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
Insert Length: 3883 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 329.
                                                                                                                                                                                                                                                                                                                                                                                                    tx62f10.x1 NCI CGAP Ut1 Homo sapiens cDNA clone IMAGE:2274187 3' similar to TR:075473 075473 ORPHAN G PROTEIN-COUPLED RECEPTOR HG38.
                                                                                                                                                                                                     CCAACTGCATCCTAAACTGCCCTGTGGCTTTCTTGTCCTTCTCCTCTTAATAAACCTTA 2380
                                                       CCCTTTGCTTCCTCATGATGACCATTGCCTACAAGCTCTACTGCAATTTGGACAAGG 2260
                                                                                                                              GAGACCTGGAGAATATTTGGGACTGCTCTATGGTAAAACACATTGCCCTGTTGCTCTTCA 2320
254 CTTTGCCTTTTGGGGAGCCCAGCACCATGGCTACATGGTCGCTCTCATCTTGCTCAATT 195
                                                                          194 CCCTTTGCTTCCTCATGATGACCATGCCTACACCAAGCTCTACACTGCAATTTGGACAAGG 135
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//note="Organ: ulerus; Vector: pCMV-SPORT6; Site 1: Sall;
Site 2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Life Technologies catalog #:
                                                                                                                                                  CCAACTGCATCCTAAAACTGCCCTGTGGCTTTCTTGTCCTTCTTCTTTAATAAACCTTA 15
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 358)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/lab host="DH10B"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:2274187"
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2044 AAAGTAATCATTTTGCTCTGTGCCCTGCTGGCCTTGACCATGGCCGCAGTTCCCCTGCTG 2103

Matches 354; Conservative

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 494)

SR Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Lennon,G., Marra,M., Martin,J., While,T., Materston,R., Tan,F., Theising,B., White,Y., While,T., Waterston,R. and Wilson,R.

NashU-Merck EST Project 1997

Unpublished (1997)

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Washington University School of Medicine
4444 Porset Park Parkway, Box 8501, St. Louis, MO 63108

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Fax: 314 286 1800

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Fax: 116 260watson.wustl.edu

This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 471.
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AAAGTAATCATTTTGCTCTGTGCCCTGCTGGCCTTGACCATGGCCGCAGTTCCCCTGCTG 299
                                                                                                                                                                                                                                      238 ACCATGGGCTACATGGTCGCTCTCATCTTGCTCAATTCCCTTTGCTTCCTCATGATGACC 179
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (base 1 to 539)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

The Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmal: Capabb-ramail.nih:gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CODA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies of General General Cound through the I.M.A.G. Econoctium/Link at:

www-bio.lln.gov/bbrp/image/image/image.html
Insert Length: 960 Std Error: 0.00

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       Length 494;
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     Score 345; DB 1; I
Pred. No. 8.3e-178;
0; Mismatches 0;
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High quality sequence etop: 405.
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                                                                     /tissue type="poorly-differentiated endometrial
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.45 kb. Life Technologies catalog #:
11541-018"
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/mol_type="mRNA"
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/clone="IMAGE:2208807"
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Heu S.Y., Liang S.-G., Heuch A.J.W.;

"Characterization of two LGR genes homologous to gonadotropin and thyrotropin receptors with extracellular leucine-rich repeats and a G protein-coupled, seven-transmembrane region.";

Mol. Endocrinol. 12:1830-1845(1998).

-I FUNCTION: Orphan receptor. It may be an important receptor for signals controlling growth and differenciation of specific embryonic tissues (By similarity).

-I SUBCELLULAR LOCATION: Integral membrane protein.

-I TISSUB SPECIFICITY: Expressed in skeletal muscle, placenta, spinal cord, and various region of brain.

-I SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

-I SIMILARITY: Contains 17 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Leucine-rich repeat-containing G protein-coupled receptor 5 precurso (Orphan G protein-coupled receptor Gorphan G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98308104; PubMed=9642114; DOI=10.1006/bbrc.1998.8774; MEDLINE=98308104; PubMed=9642114; DOI=10.1006/bbrc.1998.8774; McDonald T., Wang R., Bailey W., Xie G., Chen F., Caskey C.T., Liu Q "Identification and cloning of an orphan G protein-coupled receptor the glycoprotein hormone receptor subfamily."; Biochem. Biophys. Res. Commun. 247:266-270(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Q68ci3
Q93yt3
Q8k7x8
Q8p1f7
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Q6ant4
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MEDLINE=99065210; PubMed=9849958; DOI=10.1210/me.12.12.1830;
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09DG06
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Q8UHZ5
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Q7ZX47
Q9W761
Q9XVN1
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Q7XNV7
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075473; Q9UP75;
28-FEB-2003 (Rel. 41, Created)
                                                   SEQUENCE FROM N.A.
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 NCBI_TaxID=9606;
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            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                               protein search, using frame_plus_n2p model
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; AF061444; AAC77911.1; -...

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MIM; 606667; -...

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GO; GO:000190; F:G-protein coupled receptor protein signalin. .; TAS.

RO; GO:000191; F:G-protein coupled receptor protein signalin. .; TAS.

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InterPro; IPR00121; Gphrm. receptor.

InterPro; IPR00121; LRR LYP.

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PROSITE; PS00237; GPKRHODOPSN.

PROSITE; PS00262; G-PROTEIN RECEP FI 1; FALSE NEG.

PROSITE; PS00237; GPROTEIN RECEP FI 2; 1.

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Name-Gpr49;
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN-CSTBL/64; TISSUE-Head;
MEDINE-99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
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QBC8A7;
QBC8A7;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
O1-MAR-2004 (TrEMBLrel. 23, Last sequence update)
O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:Cl30018C02 product:G protein-coupled receptor 49, f
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Adachi J., Aizawa K., Hanagaki T., Hara A., Hashizume W.,
An Indeani K., Indiani Y., Itoh M., Kagawa I., Kasukawa T.,
An Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M.,
Katoh H., Kawai J., Kojima Y., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Oksaka Y.,
Saito R., Saito R., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                           STRAIN=C55BL/6J; TISSUE=Head;
The FANTOM Consortium,
the RANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE-Head;

MEDLINE=20499374; PUMPGd=11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare fiull-length cDNA libraries for rapid discovery of new genes.";

Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CSTBL/6J; TISSUE=Head;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasakin N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunnoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara B., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., RIKIS integrated sequence analysis (RISA) system-184-format Genome Res. 10:1757-1771(2000).
                                                        SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Head;
STRAIN=C1098/35055500;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM COMSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
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InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003591; LRR_typ.
Pfam; PF01462; LRRNT; 1.
Pfam; PF00560; LRR 1; 9.
PRINTS; PR00019; LEURICHRPT.
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SMART; SM00369; LRR_TYP; 6.
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363

Length:

9.1e-43

Alignment Scores: Pred. No.:

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25-072-2004 (Rel. 45, Last annotation update)
Leucine-rich repeat-containing G protein-coupled receptor 5 precursor (G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-99121227; PubMed-9920770; DOI=10.1006/bbrc.1998.9882;
Hermans G., Methner A., Schaller H.C., Hermans-Borgmeyer I.;
"Identification of a novel seven-transmembrane receptor with homology to glycoprotein receptors and its expression in the adult and developing mouse.";
Biochem. Biochem. 199499.

-i- FUNCTION: Orphan receptor. It may be an important receptor for signals controlling growth and differenciation of specific
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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HSSP; Q9BZR6; 1OZN.
MGD; MGI:1341817; Gpr49.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                      MOUSE
                                                                                                                                                                         667
                                                                                                                                                                                                                                                             243
                                        Query Match:
DB:
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1921 GGTTTTTTGTCCATTTTTGCTTCAGAATCATCTGTTTTTCCTGCTTACTCTGGCAGCCCTG 1980
      Malek M., Ciobanu D.C., Rothschild M.F.;

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

GO; GO:0016201; C:integral to membrane; IEA.

GO; GO:0016500; F:protein-hormone receptor activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0007186; P:Grotein coupled receptor protein signalin. .; IEA.

InterPro; IPR000276; GPCR Rhodpsn.

InterPro; IPR001313; GpArma receptor.

PRINTS; PR001313; GLYCHORMONĒR.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OSHBX8; Q96K69;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Leucine-rich repeat-containing G protein-coupled receptor 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEQUENCE FROM N.A.
MEDLINE=203088592; PubMed=10935549; DOI=10.1210/me.14.8.1257;
Hsu S.Y., Kudo M., Chen T., Nakabayashi K., Bhalla A.,
van der Spek P.J., van Duin M., Hsueh A.J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 AA; 15250 MW; 01AE345327EB3586 CRC64;
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27
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
G protein-coupled receptor 49 (Fragment).
Sus scrofa (Pig).
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                           147 AA
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                                                                    727 TACAATAACCTTGATGAATTCCCCACTGCAATT
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NON TER
NON TER
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InterPro; IPR000276; GPCR_Rhodpan.

InterPro; IPR001311; Gphrmn_receptor.

R InterPro; IPR001311; IRR_Nerm.

InterPro; IPR001311; IRR_Nerm.

InterPro; IPR001321; IRR_Nerm.

InterPro; IPR001321; IRR_Nerm.

InterPro; IPR001321; IRR_Typ.

R Pfam; PP001601; IRR_T; 16.

R Pfam; PR00137; GPCRHUDODPSN.

R RINTS; PR00137; GPCRHUDODPSN.

R RINTS; PR00137; GPCRHUDODPSN.

R RMART; SM0013; ILRR_TYP; 8.

SMART; SM0013; ILRR_TYP; 8.

SMART; SM0013; IRR_TYP; 8.

R PROSTITE; PS00237; G PROTEIN RECEP_F1_1; FALSE_NEG.

R PROSTITE; PS00227; G PROTEIN RECEP_F1_2; 1.

M G-Protein coupled receptor; Glycoprotein; Leucine-rich repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   726
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Leudine-rich repeat-containing
coupled receptor 5.
Extracellular (Potential).
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553167C6C0AAE253 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytoplasmic (Potential).
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LIRR 4.
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                                                                                                                                                                                                                                                                                                                          TISSUE—Nammary gland;

TISSUE—Nammary gland;

TURNIE—Nammary gland;

TURNIE—Nammary gland;

TURNIE—Nammary gland;

TO Deal T., Sulviki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

A Cat T., Sulviki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

A Makamateu A., Hayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

A Mamanoto J.-I., Salto M., Yasudi T., Isono Y., Nakamura Y.,

A Namanoto J., Kamihari M., Kanda K., Yokoi T., Furuya T., Kikkawa B.,

Shiratori A., Sudo H., Hosolri T., Kaku Y., Kodaira H., Kondo H.,

Shiratori A., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,

A Manazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,

Rusano J., Kanahori K., Takahashi Pujii A., Hara H., Tanaka T.,

Kusano J., Kanahori K., Takahashi-Pujii A., Hara H., Tanase T.-O.,

Rusano J., Kanahori K., Yuuki H., Oobhima A., Sasaki N., Aotsuka S.,

Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,

Nomura Y., Togiya S., Komai F., Hara R., Takeuchi W., Sano S.,

Nomiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,

A Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

A Hishigaki H., Watanabe K., Kumagai A., Itakura S., Fujiwara T.,

A Nakagawa S., Senoh A., Mizoguchi H., Takemoto M., Kawakami B.,

Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fujiwara T.,

A Nakagawa S., Senoh Y., Noguchi S., Itoh T., Shigeta K., Senba T.,

A Nakagawa S., Senoh W., Hata H., Watanabe M., Komatsu T.,

A Nakajaki H., Wakaima Y., Matauna Y., Noguchi S., Itoh T., Shigeta K., Saabai T.,

A Nakashata A., Hikiji T., Kobatake N., Inagaki H., Ikae M., Nakajawa Y., Nakajima Y., Nakasiki M., Nakajima Y., Nakasiki M., Nakas
                                                                                                                             SEGUENCE OF 406-828 FROM N.A. MEDIALIDIE/S0014-5793(02)02775-8; MEDILINE-22040266; PubMed-12044878; DOI-10.16/S0014-5793(02)02775-8; Takeda S., Kadowaki S., Haga T., Takaeu H., Mitaku S.; "Identification of G protein-coupled receptor genes from the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nat. Genet. 36:40-45(2004).
--- FUNCTION: Orphan receptor.
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
--- SIMILARITY: Contains 11 leucine-rich (LRR) repeats.
"The three subfamilies of leucine-rich repeat-containing G protein-coupled receptors (LGR): identification of LGR6 and LGR7 and the signaling mechanism for LGR7,";

MOI. Endocrinol. 14:1257-1271(2000).
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InterPro; IPR002131; Gphrmn_receptor.
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EMBL; AK027377; BAB55071.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001611; LRR.
InterPro; IPR003591; LRR_typ.
Pfam; PR00560; LRR; 12.
PRINTS; PR00373; GLYCHORMONER.
PRINTS; PR00237; GPCRHODOPSN.
PRINTS; PR00019; LEURICHRPT.
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                                                                                                                                                                                                                                                                                                               SEQUENCE OF 431-828 FROM N.A.
                                                                                                                                                                                                                                       genome sequence.";
FEBS Lett. 520:97-101(2002).
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"The thre coupled I
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G_PROTEIN RECEP_F1_1; FALSE NEG.
G_PROTEIN_RECEP_F1_2; FALSE_NEG.
receptor; Glycoprotein; Leucine-rich repeat; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Clark H.F., Gurney A.L., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Poster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 853 ACAATACATTCTANGACAATCCCATCCAATTTGTTGGGAGATCTGCTTTTCAA 906
                                                                                                                                                                                                                                                                                                                        By similarity.

N-linked (GlCNAc. . .) (Potential).

N-linked (GlCNAc. . .) (Potential).

CSPTP -> MISPT (in Ref. 2).

W -> R (in Ref. 3).

FASHV -> LLHTY (in Ref. 1).

W; 1BS971445AA2D8B4 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                              (Potential).
                                                                                                                                                                 Extracellular (Potential).
7 (Potential).
Cytoplasmic (Potential).
Poly-Gly.
                                          Extracellular (Potential).
                                                                                                     Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential).
                                                                       2 (Potential).
Extracellular (Potential)
                                                                                                                                     5 (Potential).
Cytoplasmic (Potential).
6 (Potential).
                                               (Vtoplasmic (Potential).
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Last annotation update)
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Matches:
Conservative:
Mismatches:
                                                                                             3 (Potential)
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LERR 4.
LERR 5.
LERR 6.
LERR 7.
LERR 8.
LERR 9.
LERR 10
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                                                                                                                                                                                                                                                                                                                                                                                        89301 MW;
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05-JUL_2004 (TrEMBLrel. 27,
05-JUL_2004 (TrEMBLrel. 27,
Gonadotropin receptor.
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PROSITE; PS00237; G
PROSITE; PS50262; G
G-protein coupled r
Transmembrane.
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TRANSMEM
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CONFLICT
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REPEAT
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                                                                                   DOMAIN
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SEQUENCE FROM N.A.
TISSUE=Blood;
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DB:
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        The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";

Bloinformatics assessm
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A Klausher R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M. J., Ubdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Muhing M., Madan A., Young A.C., Shevchenko Y., Buikfard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        853 ACAATACATTTCTATGACAATCCCATCCAATTTGTTGGGAGATCTGCTTTTCAA 906
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A. Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D. Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D57DD7A9DBB555F4 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            915 AA; 99265 MW;
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PRINTS; PRO013/7; GPCRHODOPSN.
PRINTS: PRO0019; LEURICHRPT.
SMART; SMO0365; LRR. SD22; 5.
SMART; SM00369; LRR_TYP; 14.
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18.00
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1.98$
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Best Local Similarity:
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086VU0
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0D 01-U
0DT 01-U
0DT 01-M
0DT 01
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016500; F:protein-hormone receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
InterPro; IPR00131; GPCR Rhodpsn.
InterPro; IPR00131; GpArmu_receptor.
InterPro; IPR001611; IER.
InterPro; IPR001591; IER_typ.
Pf00560; IRR_1; 15.
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.L., Skalska U., Smailus D.E., Schmerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTS20631 (Fragment).
Name=VTS20631;
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                      GO; GO:001601; C:integral to membrane; IEA.
GO; GO:0016500; F:protein-hormone receptor activity; IEA.
GO; GO:00105500; F:protein-hormone receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
InterPro; IPR002131; GPCR. Rhodpsn.
InterPro; IPR002131; Gphrmn_receptor.
InterPro; IPR001319; LRR_typ.
Pfam; PP00560; LRR_1; 15.
PRINTS; PR00373; GLYCHORMONER.
PRINTS; PR00373; GCYCHORMONER.
PRINTS; PR00193; GCYCHORMOPEN.
SMART; SM00369; LRR_TYP; 8.
                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCC47905; AAH47905.1; -.
HSSP; Q9RZ6, 1P8T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Okaze H., Hayashi A., Kozuma S., Saito T.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO49405; BAB39854.1; -.
HSSP; P25417; 1D0B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                541D6746DAB06813 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
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Gaps:
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PRINTS; PR00237; GPCRHODOPSN
PRINTS; PR00019; LEUBICHPT.
SMART; SM00369; LRR_TYP; 8.
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NCBI_TaxID=9606;
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Q8N537;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; Manlaysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Retina;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=CS7BL/6G; TISSUE=Retina;
MEDLINE=9927923; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                  ThrileHisPheTyrAspAsnProlleGlnPheValGlyArgSerAlaPheGln 263
                                                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult retina cDNA, RIKEN full-length enriched library,
clone:A930009A08 product:G PROTEIN-COUPLED RECEPTOR LGR4 homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIM-C57BL/GJ; TISSUE-Retina;
MEDLINE-20530913; Pubmed=11076861; DOI=10.1101/gr.152600;
MEDLINE-20530913; Pubmed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                   853 ACAATACATTTCTATGACAATCCCATCCAATTTGTTGGGAGATCTGCTTTTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Retina;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
            4C3364ADEA89C463 CRC64;
                                                 928
0 0 0
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                                                                           Conservative:
Mismatches:
Indels:
                                                  Length:
Matches:
                                                                                                                                                                                                                                              878
                                                                                                                Gaps:
                                                                                                                                         (1-928)
                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                             PRT;
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STRAIN=C57BL/6J; TISSUE=Retina;
          100487 MW;
                                                                                                                                           US-10-751-736-21 (1-2724) x Q9BYD7
                                              1.29e-08
18.00
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100.00$
                                                                                                                                                                                                                                                                     (TrEMBLrel. 23, (TrEMBLrel. 23,
                                                                                                                                                                                                                                             PRELIMINARY;
1
928 AA;
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                                                                         Percent Similarity:
Best Local Similarity:
                                     gnment Scores:
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                                                                                                                                                                                                                                                                                                                                                  Name=Gpr48;
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                                                                                                    Query Match:
DB:
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MGD; MGI:1891468; Gpr48.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016500; F:protein-hormone receptor activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:000486; F:receptor activity; IEA.

GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

InterPro; IPR00276; GPCR_Rhodpsn.

InterPro; IPR002131; Gphrmn_receptor.
                                                                                                                                                                                           Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa T., Koda M., Koya S., Katoh H., Kawai J., Kojima Y., Kondo S., Komno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinaqawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

R. RMBL, AKO44357; BAC31882.1; -.
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TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 1844 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
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Mammalia; Butheria; Primates; Catarrhini; Hominidae;
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22, Last sequence update)
26, Last annotation update)
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PRINTS; PRO0237; GPCRHODOPSN.
PRINTS; PRO0019; LEURICHRPT.
SMART; SMO0369; LEURICHRPT.
PROSITE; PSS0262; G_PROTEIN RECEP_F1_2; 1.
PROSITE; PSS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
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                                                                                                                                                                               STRAIN=C57BL/6J; TISSUE=Retina;
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InterPro; IPR003591; LRR typ.
InterPro; IPR007087; Znf_C2H2.
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01-OCT-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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Pfam; PF00560; LRR_1;
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MIM; 606666;
                                                   SEQUENCE
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    Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
An expletion M., Moore T., Max S.I., Wang J., Hsieh F.,
Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Garsen M.B., Bonaldo M.P., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Wickernan K.J., Maake J.A., Gubbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Rodiques S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Jones S.J., Marra M.A.,
Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                          GO; GO:001601; C:integral to membrane; IEA.

GO; GO:001601; C:integral to membrane; IEA.

GO; GO:0010186; P:protein-hormone receptor activity; IEA.

GO; GO:0010186; P:G-protein coupled receptor protein signalin. . ; IEA.

InterPro; IPR001376; GFCR. Rhodgan.

InterPro; IPR00131; Gphrmn_receptor.

InterPro; IPR001611; IER.

InterPro; IPR001051; LER.

InterPro; IPR001087; Znf_C2H2.

Pfam; PF00162; LERNIT; 1.

Pfam; PF0162; LERRIT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGR4 HUMAN STANDARD; PRT; 951 AA.
Q9BXB1; Q9NYD1;
Q9FB51; Q9NYD1;
28-FB8-2003 (Rel. 41, Created)
28-FB8-2003 (Rel. 45, Last sequence update)
Loucine-rich repeat-containing G protein-coupled receptor 4 precursor (G protein-coupled receptor 48).
Name=GPRA8; Synonyms=LGR4;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC033039; AAH33039.1; -.
HSSP; P25147; 1D0B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR TYP; 5.
PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.
PROSITE; PS00269; ZINC PINGER C2H2 1; UNKNOWN 1.
SEQUENCE 927 AA; 101676 MW; C7B2P0C40ES84GE8 CRC64;
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13
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                                                                                                                                                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00373; GLYCHORMONER.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR00019; LEURICHRPT.
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HSSP, Q9BZR6; 10ZN.
RGD; 628615; Gpr48.
InterPro; IPR000276; G
InterPro; IPR002131; G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Leucine-rich repeat-containing G protein-coupled receptor 4 precursor.
Mame=Gpr48; Symonym=Lgr4;
Rattus norvegicus (Rat).
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Б
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99065210; PubMed=9849958; DOI=10.1210/me.12.12.1830; Hau S.Y., Liang S.-G., Hsueh A.J.W.; Hau S.Y., Liang S.-G., Hsueh A.J.W.; Hau S.Y., Liang S.-G., Hsueh A.J.W.; Characterization of two LGR genes homologous to gonadotropin and thyrotropin receptors with extracellular leucine-rich repeats and a protein-coupled, seven-transmembrane region."; Mol. Endocrinol. 12:1830-1845(1998).
-!- FUNCTION: Orphan receptor.
-!- SIMCLALIGAR LOCATION: Integral membrane protein.
-!- SIMLIARITY: Belongs to the G-protein coupled receptor 1 family.
-!- SIMLIARITY: Contains 15 leucine-rich (LRR) repeats.
                                                                                                                By similarity.
N-linked (GlCKNc. .) (Potential).
F -> S (in Ref. 1; AAF68989).
L -> P (in Ref. 1; AAF68989).
L -> S (in Ref. 1; AAF68989).
L -> S (in Ref. 1; AAF68989).
                                                                                                                                                                                                                                                                                                                      622 AACCTCTCCAGCTTGGTAGTTCTACATCTCCATAACAAT 660
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Matches:
Conservative:
Mismatches:
Indels:
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LER 5.
LER 6.
LER 7.
LER 9.
LER 10.
LER 11.
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Best Local Similarity:
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Pred. No.:
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DISULFID
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CARBOHYD
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0922H4;
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InterPro; IPR00131; Gphrmn_receptor.

DR InterPro; IPR00131; Gphrmn_receptor.

DR InterPro; IPR000372; LRR Nterm.

DR InterPro; IPR000372; LRR Nterm.

DR Pfam; PP00001; 7tm 1; 1.

DR Pfam; PP01462; LRRN; 15.

DR PRINTS; PR00137; GPCRHODOPSN.

DR PRINTS; PR00137; GPCRHODOPSN.

DR SWART; SM00013; LRRNT; 1.

DR SWART; SM00013; LRRNT; 5.

DR SWART; SM0013; LRRNT; 1.

DR SWART; ENDOSTER TYP; 5.

DR SWART; ENDOSTER TYP; 5.

DR SWART; MO0149; LRR TYP; 5.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Glycoprotein; Leucine-rich repeat; KW Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                             Leucine-rich repeat-containing G protein-
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(Potential).
(Potential).
(Potential).
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6 (Potential).
Extracellular (Potential).
7 (Potential).
Cytoplasmic (Potential).
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2 (Potential).
2 (Potential).
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3 (Potential).
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6 (Potential).
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5 (Potential).
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Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               622 AACCTCTCCAGCTTGGTAGTTCTACATCTCCATAACAAT 660
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EDD56AC072123461
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Matches:
Conservative:
Mismatches:
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LER 6.
LER 7.
LER 9.
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LER 11.
LER 12.
LER 13.
LER 13.
LER 14.
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LER 16.
N-linked (GlCN)
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Q8R301
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N SEQUENCE FROM N.A.

MEDLINE-22584407; PubMed-12679517; DOI=10.1073/pnas.0230374100;

N Vassilatis D.K., Hohmann J.G., Zeng H., Li F., Ranchalis J.B.,

N Anstruct M.T., Brown A., Rodriguez S.S., Weller J.R., Wright A.C.,

N Hording D.K., Galtanaris G.A.,

The G protein-coupled receptor repertoires of human and mouse.";

The G protein-coupled receptor repertoires of human and mouse.";

The G protein-coupled receptor repertoires of human and mouse.";

N Hording NA255619; AA085131.1;

N HSSP; P25146; 106T.

DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro; IPR001611; LRR.

DR InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22584407; PubMed=12679517; DOI=10.1073/pnas.0230374100; Vassilatis D.K., Hohmann J.G., Zeng H., Li F., Ranchalis J.E., Vasctrud M.T., Brown A., Rodriguez S.S., Weller J.R., Wright A.C., Bergmann J.E., Gaitanaris G.A.

"The G protein-coupled receptor repertoires of human and mouse."; Proc. Natl. Acad. Sci. U.S.A. 100:4903-4908(2003).

EMBL; A725562; AAO85074.1; -...
GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Fragment).
Nus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Leucine-rich repeat-containing G protein-coupled receptor 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4D3559000D69C67E CRC64;
    AsnLeuSerSerLeuValValLeuHisLeuHisAsnAsn 211
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111
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                                                                                                                                                01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) G protein-coupled receptor GPR48 (Fragment).
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                      134
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                                                                                                                            (TrEMBLrel. 24, Created)
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PRINTS; PR00019; LEURICHRPT.
SMART; SM00369; LRR TYP; 2.
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                                                                                                                                                                                                                   Mus musculus (Mouse)
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Pred. No.:
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Q80UBB
AC Q80UBB
AC Q80UB
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DT 
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                                                                Score:
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-Czech II; TISSUE-Mammary tumor;

MEDLINE-2238257; PubMed=1247932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

A Rabaren R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Rischul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhata N.K.,

A Hopking R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Minting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:2441805; Lgr6.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016500; F:protein-hormone receptor activity; IEA.
GO; GO:0007186; P:protein-coupled receptor protein signalin. . .; IEA.
InterPro; IPR00276; GPCR_Rhodpsn.
InterPro; IPR02131; Gphrmn_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC026896; AAH26896.1; -
1
162
17608 MW; C593128C551FB824 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     459 AA; 47889 MW; F0100BF073E81762 CRC64;
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Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                  Indels:
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                                                                                                                                                                                                                                                                                                                                                      US-10-751-736-21 (1-2724) x Q80UB8 (1-162)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                            0.283
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162 1
162 AA;
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                                                                                                                                                                                                                                         Best Local Similarity:
                                                                                                                                                                                                       Percent Similarity:
                                                                                                                   Alignment Scores:
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US-10-751-736-21 (1-2724) x Q8R301 (1-459)

Search completed: July 13, 2005, 03:56:52 Job time: 284.5 secs

AF257182 Homo sapi BV208561 GPR49 209 BD135243 Novel mam AX827367 Sequence

AXS49295 Sequence AB049405 Homo sapi AC126127 Rattus no AC132780 Rattus no CQ870634 Sequence BC047905 Homo sapi CQ840811 Sequence AX938119 Homo sapi AX95300 Sequence AC126943 Mus muscu AX451929 Sequence AC126943 Mus muscu AX451929 Sequence AX078359 Sequence AX078359 Sequence BD07570 G protein AX549242 Sequence

APOGE1443 Rattus no BC033039 Homo sapi E42215 Novel gonad AX016185 Sequence AF190501 Homo sapi E42917 Novel gonad

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Minimum | Maximum |

Database

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Result Š 180

240

OM nucleic

Run on:

Sequence:

Searched:

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Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGGGCAGCTCTCCCAGGTCTGTGTTGCTGAGGGCCTGCCCCACACACTGTCATTGC 120
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGCCCGACGGCAGGATGTTGCTCAGGGTGGACTGCTCCGACCTGGGGCTCTCGGAGCTG
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PE Corporation (NY) (US)
Location/Qualifiers
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Sequence 7300 from Patent WO02068579.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 2724;
llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches

    .2724
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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BC033039
E42915
AXS49295
AB049405
AC132780
AC132780
AC132780
BC047905
AX926300
AX358119
AX926300
AX451929
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Matches 2724;
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VERSION
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AUTHORS
TITLE
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AX308745 Sequence
AX49136 Sequence
AX658241 Sequence
AX658241 Sequence
AX658241 Sequence
AX562006 Homo sapi
BD075815 G protein
AR47625 Sequence
AX308744 Novel mam
AF110818 Mus muscu
AK07539 Homo sapi
AX301824 Sequence
AX301822 Sequence
AX301822 Sequence
AX301833 Sequence
AX301831 Sequence
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AX301831 Sequence
                                                                                                         July 12, 2005, 11:03:57; Search time 12213.8 Seconds (without alignments) 10806.757 Million cell updates/sec
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                                                                                                                                                                                                      1 atggacacctcccggctcgg......catttgtcccatgtctctaa 2724
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              version 5.1.6
- 2005 Compugen Ltd.
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AF062006
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                  GenCore (c) 1993 -
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seq length: 200000000
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2401	2461 AICHGAILCHCACHTAAGAASAALIGGIGAGCCGAGCAAACCAACTACGAGCAACCTACGAGCAACCTAACGAGCAACCTAACGAGCAACCTAACGAGCAACCTACGACAACCTACGAGCAACCTACGAGCAACCTACGAGCAACCTACGAGCAACCTACGAGCAACCTACGAGCAACCTACGACAACCTACGACAACCTACGAACCAACC	Qy 2521 TGGACAAGATCAAAACACCCAAGCTTGATGAATTAACTCTGATGATGATGTGGAAAAACAG 2580		2641 CCTCCCAGTTCCGTGCCATCACCACCACCACCACCACCACCACCACCACGTTCCGTGCCATCACCACACACA	Oy 2701 GTGGCATTGTCCCATGTCTCTAA 2724	RESULT 3 AR308745 LOCUS AR308745 AR3087	AR308745 AR308745.1 GI:31700274	SOURCE Unknown. ORGANISM Unknown. Unclassified. REFERENCE 1 (bases 1 to 2724)		FARIONES LOCALLON, VALLILLES 12724 /organism="unknown" /mol_type="genomic DNA"	score 2724; DB 6; Length 2724; pred. No. 0;	Matches 2/24; Conservative 1 ATGACACCTCCCGGCTCC		121 GAGCCCGACGGATGTTGCTCAGGTGTGTTGCTCAGGCCCCCCCC	GAGCCCGACGGCAGGATGTTGCTCAGGGTGGACTTGCTCCGAACTTGGGGTCTGGGGTGGACTTGCAGCTTCGAACACTTGGAGGTGAGACAACATAGGAGGTGAGAACAACATAGAACAAACA	241 CTGCTCCGAATCCCCTGCTCCCCTGCTTCAAGAGAGTTACGTCTTGCGGGAAAC	301 GCTCTGACATTCCCAAGGAGGAGCTTCATGAGGAGGAGTTTACATTATG	Db 301 GCTCTGACATACATTCCCAAGGGAGCATTCACTGGCCTTTACAGTCTTAAAGTTCTTATG 360 OV 361 CTGCAGAATAATCAGCTAAGCTAACCGACACAAAGAACTTGCGAAAGTTTGCGAAAGCTT 420
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KDAGMFQAQDERDLEDPLLDPEEDLKALHSYQCCSPSPGPFKPCEHLLDGWLIRIGWY
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VIILLCALLALTMAAVPLLGGSKYGASPLCLPLPFGEPSTWGYWALILLNSLCFLMM
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EVIKFILLVVVPLPAGLINPLILIFNPHFKEDLVSLRKQTYVWTRSKHPSLWSINSDD
VEKQSCDSTQALVTFTSSSITYDLPPSSVPSPAYPVTESCHLSSVAFVPCL
                                                                                                                                           AF062006 2880 bp mRNA linear PRI 31-JUL-1998
Homo sapiens orphan G protein-coupled receptor HG38 mRNA, complete
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2880)
McDonald,T., Wang,R., Bailey,W., Xie,G., Chen,F., Caskey,C.T. and
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MCDONald,T., Wang,R., Bailey,W. and Liu,Q.
Direct Submission
Submitted (29-APR-1998) Human Genetics, Merck Research Labs,
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                  Liu, O.
Identification and cloning of an orphan G protein-coupled of the glycoprotein hormone receptor subfamily
Biochem. Biophys. Res. Commun. 247 (2), 266-270 (1998)
98308104
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2724; Conservative 0; Mismatches
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Location/Qualifiers
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/organism="Homo sapiens"
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/chromosome="12"
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In (bases 1 to 4559)

Is liu,0., Berly,W.J. and Macdonald,T.P.

G protein-coupled glycoprotein hormone receptor HG38

D patent: JP 2001517441-A 1 09-OCT-2001;

Extent: JP 2001517441-A 1 09-OCT-2001;

D patent: JP 2001517441-A/1

PN JP 2001517441-A/1

PN JP 2001517441-A/1

PN JP 200151741-A/1

PN JP 200151741
                                            2509 ATCTTGTTCAATCCTCACTTTAAGGAGGATCTGGTGAGCCTGAGAAAGCAAACCTACGTC
                                                                                                                                                                                                                                                                                                CCTGTGGCTTTCTTGTCCTTCTCCTCTTAATAAACCTTACATTTATCAGTCCTGAAGTA
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G protein-coupled glycoprotein hormone receptor HG38
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G protein-coupled glycoprotein hormone receptor HG38.
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Db 2602 CCTGTGGCTTTCTTCTCTCTTTAATAAACCTTACGTTCTCTGAGTA 2661 Oy 2401 ATTAAGTTTATCCTTCTGGTGGTGGTTCCTGATTCTCTCTC	RESULT 9 AR308754 LOCUS DEFINITION Sequence 277 from patent US 6555339. ACCESSION AR308754.1 GI:31700283 VERSION AR308754.1 GI:31700283 KEYWORDS ORGANISM Unknown. ORGANISM Unknown. ORGANISM Unknown. TITLE Non-endogenous, constitutively activated human protein-coupled receptors JOURNAL Patent: US 6555339-A 277 29-APR-2003; FEATURES Incarion/Qualifiers SOURCE Incarion/Qualifiers Incari	Query Match 99.9%; Score 2720.8; DB 6; Length 2724; Best Local Similarity 99.9%; Pred. No. 0; 0 Gaps 0; Qy 1 ATGGACACCTCCGGCTCGGTGCTCCTGCTGCTGCTGCTGCTGCGCGCCC 0 1 1 Db 1 ATGGACACCTCCGGCTCGGTGTGCTCTTGCTTGCTGCTGCTGCTGCT
1261 TIGCCATCCCTAATAAAGCTGACCTATCGTCCACCTCCTGTCGTCTTTTCCTATAACT 1320	1811	1991 GAGCGTGGGTTCTCTGTGAAATTTCTGCAAAATTTGAAAGGTAGCTCCATTTTCTGC 2040

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Pred. No. 0;
0; Mismatches
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                                                                                                                                               Best Local Similarity 99.9
Matches 2721; Conservative
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VIILLCALLALTWAAVPLLGGSKYGASPLCLPLPFGEPSTWGYMVALILLNSLCFLAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MDTSRLGVLLSLPVLLQLATGGSSPRSGVLLRGCPTHCHCEPDG
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Haus, S.Y., Liang, S.G. and Hsueh, A.J.
Characterization of two LGR genes homologous to gonadotropin and thyrotropin receptors with extracellular leucine-rich repeats and gorocein-coupled, seven-transmembrane region
Mol. Endocrinol. 12 (12), 1830-1845 (1998)
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Catarrhini, Hominidae, Homo.
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Hsu,S.Y., Liang,S.G. and Hsueh,A.J.W.
Direct Submission
Submitted (S-APR-1998) Gyn/Ob, Stanford University, 300 Pasteur
Dr., Stanford, CA 95305-5317, USA
Location/Qualifiers
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                                                                              TGGACAAGATCAAAACACCCCAAGCTTGATGTCAATTAACTCTGATGTTGAAAAAACAG
                                                                                                                                                                         TCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTTATGACCTG
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     ATCTTGTTCAATCCTCACTTTAAGGAGGATCTGGTGAGCCTGAGAAAGCAAACCTACGTC
                                                     TGGACAAGATCAAAACACCCCAAGCTTGATGTCAATTAACTCTGATGATGTCGAAAAAAGG
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protein_id="AAC77911.1"
db_xref="GI:3885472"
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/mol type="mRNA"
/db_xref="taxon:9606"
1. 2724
                                                                                                                                                                                                                                                                                                                                          GTGGCATTTGTCCCATGTCTCTAA 2724
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Mammalia; Eutheria; Primates;
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C Novel mammalian G protein-coupled receptor having CC extracellular
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| /organism='Homo sapiens (human)'.
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Biochem. Biophys. Res. Commun. 254 (1), 273-279 (1999)
                                                                                                                                                                                                                                                 Mus
                                                                                                                                                                  AF110818 3115 bp mRNA linear ROD 11-FEB-19:
Mus musculus orphan G protein-coupled receptor FEX mRNA, complete
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                       GATGATGTCGAAAAACAGTCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCC
                                                                AGCATCACTTATGACCTGCCTCCCAGTTCCGTGCCATCACCAGCTTATCCAGTGACTGAG
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Hermey, G., Methner, A., Schaller, H.C. and Hermans-Borgmeyer, I.
Direct Submission
Submitted (33-DEC-1998) Center for Molecular Neurobiology,
Martinistr. 52, Hamburg D-20246, Germany
Location/Qualifiers
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protein id="AAD14684.1"
db_xref="GI:4262546"
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'codon_start=1
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Pred. No. 0;
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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
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Best Local Similarity 84.6%;
Matches 2304; Conservative (
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/note="cloning vector: pME18SFL3"
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and AF061444, probably caused by alternative splicing"
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SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Muc. Acids Res. 25:338-3402) similarity (expect < 1e-34) to the EST and cDNA sequences Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                               Submitted (07-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetice, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 145165)

Worley,K.C.

Direct Submission
Submitted (31-MAR-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetice, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 145165)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (01-APR-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
(bases 1 to 145165)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (23-JAN-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA ON Max 31, 2001 this sequence version replaced gi:13324671.

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 145165)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html
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(bases 1 to 145165)
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Direct Submission
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Direct Submission
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18 (Dases 1 to 1415)

19 (Dases 1 to 1415)

10 (Dases 1 to 1415)

11 (Dases 1 to 1415)

12 (Dases 1 to 1415)

13 (Dases 1 to 1415)

14 (Dases 1 to 1415)

15 (Dases 1 to 1415)

15 (Dases 1 to 1415)

16 (Dases 1 to 1415)

17 (Dases 1 to 1415)

18 (Dases 2 to Dathor, Butherburg, K., Bonnin, D., Bouck, J., Banter, P., Burattunge, H.C., Charon, T.F., Carton, T.F., Carton, T.F., Carter, M., Cavazoe, S.R., Chacko, J., Chavez, D., Charon, C., Coyle, M. D. Dathorne, S.R., Davida, M.C., Carton, T.F., Carter, M., Cavazoe, S.R., Davida, M.C., Carton, T.F., Carter, M., Carton, D., Dathorne, S.R., Davida, M. D., Dathorne, S.R., Davida, M. D., Dadon, C., Coyle, M. D. Dathorne, S.R., Davida, M. D., Dadon, C., Coyle, M. D., Dathorne, S.R., Davida, R., Davidan, C., Coyle, M. D., Dathorne, S.R., Davida, M. Daver, Cartoll, L., Dadon, D., Edward, C.C., Edward, S., Buchin, D., Maniton, M., Cartaz, P., Edward, C.C., Fagar, D., Edward, C.C., Fagar, D., Edward, C.C., Edward, S., Bantaz, P., Gadar, D., Edward, C.C., Fagar, D., Havida, J., Hale, S., Hamilton, M., Harla, T., Harria, M., Havlak, P., Hale, S., Hamilton, M., Garrel, T., Garza, M., Gall, R., Garrel, T., Garza, M., Garner, T., Garza, M., Garner, T., Hanger, J., Harria, M., Havlak, P., Hale, S., Hamilton, M., Joliver, S., Joudah, S., Joobson, B., Haven, J., Tohnson, R., Joliver, S., Joudah, S., Johnson, R., Joliver, S., Joudah, S., Johnson, R., Joliver, S., Joudah, S., Mantinez, E., Marcinez, R., Massel, L., Li, Z., Li, Lidtarge, E., Marcinez, R., Marcinez, M., Marchell, T., Mohbbat, M., Marchell, M., Sisson, M., Sisson, M., Sisson, M., Sisson, M., Sisson, M., Solott, G., Shen, H., Shim, C., Malligner, M., Mandy, M., Mandy, M., Warcher, M., Warcher, M., Warcher, M., Warchell, M., Saver, M., Sonet, M., Saver, M.
                                                                                                                                   AC078860 145165 bp. DNA linear PRI 23-JAN-2003
Homo sapiens 12 BAC RP11-186F10 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
CCATAGCAGTTCTGGCACTTACTTGTAATGCTTTGGTGACTTCAACAGTTTTCAGATCCC 1756
                                                                                                                                                                                                                                                                          1817 CGGGAGTCTCCAGTGCCGTGCTGGCTGTGGATGCGTTCACTTTTGGCAGCTTTGCAC 1876
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                        2078 CCATAGCAGTTCTGGCACTTACTTGTAATGCTTTTGGTGACTTCAACAGTTTTCAGATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2258 GACATGGTGCTGGTGGGAGAATGGGGAGAT 2289
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Homo sapiens
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145169 Summary Statistics ------

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Edited+Context
agatgragat (g) gctgtggctt
tttoggctca (c) tgcaacctcc
aaaacaacat (a) caatagataa
ttgtattgca (a) aluggcatctt
atcgttattg (t) tgttaatttt
ttttttattt (t) tattgttattt
tcatgaccta (a) tcatgtccct
ctatctctac (g) aaagaaaaga
aatggcttt (a) aaatgggccc
ctagacctg (g) aaatgaaaaga
cacatgcatt (a) gattttagt
cacatgcatt (a) gattttagt
cacatgcatt (a) atttcaggtt
gctaatttg (a) atttcaggtt
gctacact (g) agaatgaacg
gcttacact (g) agaatgaacg
gcttacact (g) aaaatgaac
gcttacact (g) agaatgaac
gcttacact (g) agaatgaac
gcttacact (g) agaatgaac
gcttacact (g) agaatgaac
gcatggtt (g) gacattaata
aaatattgtc (c) taaataaagt
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Phrap Value Range
Phrap values in estimate:
Average error rate (BCM-Phrap estimate):
Fraction of Phrap values less than 40:
Number of consensus changing edits:
Number of N's in consensus:
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1. 2004
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Incoteon="clone overlap"
complement (6. 223)
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complement (64. 698)
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complement (1023. 1077)
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complement (1228. 1482)
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complement (1228. 1201)
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complement (1740. 2021)
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complement (1740. 2021)
/rpt family="LiM9"
/rpt family="LiM9"
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/rpt family="LiM9"
/rpt family="LiM9"
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agatgtgat(a) gctggctt
tttcggctat(a) gctggctt
tttgattggcta(a) agaggatct
ttgattgat(a) agaggatct
ttgattgat(a) agagaataa
ttgttttatt(a) tgtggcatct
tcatgactat(a) tgtatttt
ttttttatt(b) tatagttaat
tcatgacta(a) aaagaaaga
aatggcttt(g) aaatgggccc
tcatgacta(n) aaagaaaga
ctagactg(n) aatgtcagg
gctaatttt(n) gattttagt
cacatgcat(n) atttcaggt
cacatgcat(n) atttcaggt
cacatgcat(n) attcaggt
cacatgcat(n) attcaggt
cacatgcat(n) attcaggt
cacatcat(n) acatcacat
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catggtgtnn (n) cacttaataa
aaatattgtc (n) taaataaagt
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/db_xref="taxon:9606"
/chromosome="12"
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/organism="Homo sapie
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                                          TGGACCATAGCAGTTCTGGCACTTACTTGTAATGCTTTGGTGACTTCAACAGTTTTCAGA
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  Length 145165;
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0
                     Indels
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Score 1090.4; DB 9
Pred. No. 2.1e-289;
0; Mismatches 1;
 Query Match
Best Local Similarity 99.9%;
Matches 1091; Conservative
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/note="unnamed protein product"
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/codon start=1
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ISSIRHLMLDDNALTEIPVRALNNLPALQAMTIALNHIRHIPDNAFQNLTSLVVLHLH
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PMGNPLLQTIHFYDNIIQPVGRSAFQYLSXLHTLSLNGATDIQEFPDLKGTTSLILT
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GEFPVTPRAVKSVLLVVLPLPACINPLITLIFNPHFRDDLRKUMPSPRSPGPLAYAAA
GELEKSSCDSTQALVAFSDVDLILEASLASLAGPPGLETYGPPSVTLISRHQPGATRLEG
NHFIBEDGTKFRONPQPPMKGELLIKAEGATLAGCGSSVGGALMPSGSLFASHL"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Novel g-protein coupled receptors and Patent: WO 0185768-A 3 15-NOV-2001; Millennium Pharmaceuticals, Inc. (US)
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/organism="Mus musculus"
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Search completed: July 12, 2005, 17:42:52 Job time : 12230.8 secs

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	Description	Aaa30770 Human G p	Abz42816 Human G p	Adc22782 Human G p	Adh14255 Human HG3	Adi32985 Human G p	Ado29923 Human GPC	Adn39796 Cancer/an	Adq80249 G protein	Adr67869 Human HG3	Adn39627 Cancer/an	Adn39530 Cancer/an	Aax23980 Human HG3	Adl12472 Human ste	Aaa30779 DNA encod	Adc22796 Human G p	Adh14269 Mutated h	Adf70582 Orphan re	Aax23981 Human HG3	Adb80463 Ovarian c	Adn39165 Cancer/an
SUMMARIES	ΩI	AAA30770	ABZ42816	ADC22782	ADH14255	ADI32985	AD029923	ADN39796	ADQ80249	ADR67869	ADN39627	ADN39530	AAX23980	ADL12472	AAA30779	ADC22796	ADH14269	ADF70582	AAX23981	ADB80463	ADN39165
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	& Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	6.66	99.9	6.66	99.8	9.66	94.2	94.2
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is substituted for an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous proline in TM6 to form a sequence X- (AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 camino acid stretch between the substituted amino acid and the Pro may be endogenous, non-endogenous, or amixture of endogenous and non-endogenous candonists. An agonists and partial agonists for use as pharmaceutical agents. The mutant proteins are also useful in research settings for elucidating the roles of the receptors in normal and diseased conditions. Antagonists for a particular GPCR are useful for treating store elucidating the roles of the receptors in normal and disease and discorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous ligands. The present sequence represents cDNA encoding a human wild-type GPCR used in an ecreptor of the invention. This was cloned and subjected to site-directed mutagenesis (SDM) to generate DNA encoding the corresponding mutant of the invention

Sequence 2724 BP; 665 A; 723 C; 554 G; 782 T; 0 U; 0 Other;

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621 TGTTCACCTTCCCCAGGCCCCTTCAAACCCTGTGAACACCTGCTTGATGGCTGGTGGTC 168
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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino caids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or constitution of a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR. and in the production of specific antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for disquising and designation immune-related diseases, immunological-related diseases, cell creating immune-related diseases, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AlDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, atherosclerosis, bacterial, fungal, protozoan or viral infections, cestecatrbritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohm's disease, graft versus host disease, parkinson's disease, multiple sclerosis, pain, psoriasis, concert, disease, parkinson's disease, multiple sclerosis, pain, psoriasis, brother disorders, theumatoid arthritis, trauma, ulcers, or hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or whypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or used in immunoassays and immunodiagnosis, ABP821523 to ABE22869 encode GPCR proceins given in ABP81675 to ABP82253 to ABE22869 encode cemplification of the present invention G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoprosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nauses; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma; ulcer; gene; des New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or 9 Gape ö DB 8; Length 2724; Sequence 2724 BP; 665 A; 723 C; 554 G; 782 T; 0 U; 0 Other; 0; Indels 100.0%; Score 2724; 100.0%; Pred. No. 0; ive 0; Mismatches Disclosure; Fig 1; 523pp; English. (LIFE-) LIFESPAN BIOSCIENCES INC. 19-DEC-2000; 2000US-0257144P. 19-DEC-2001; 2001WO-US050107. Matches 2724; Conservative Roush CL, WPI; 2003-046718/04. P-PSDB; ABP81968. autoimmune diseases. Local Similarity WO200261087-A2 Homo sapiens 08-AUG-2002. Burmer GC, -Query Match ઠ

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ACCATTGCCTACACCAAGCTCTACTGCAATTTGGACAAGGGAGACCTGGAGAATATTTGG
                                                                   CCTGTGGCCTTTCTTGTCCTTCTCCTCTTAATAAACCTTACATTTATCAGTCCTGAAGTA
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transmembrane-6 region; TM6; intracellular-3 region; IC3
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The invention relates to a method for treating a non-endogenous, constitutively active version of an endogenous human G protein-coupled receptor (GPCR) that thas a transmembrane-6 (TM6) region and an intracellular-3 (IC3) region, by substituting a specific amino acid in the TM6 region with a different amino acid, and testing for constitutive cutivity. The method is useful for reating a constitutively active version of an endogenous human GPCR that comprises a transmembrane 6 region and an intracellular loop 3 region. The altered human GPCR compounds for identification of inverse agonists or screening test compounds for identification of inverse agonists or partial agonists of GPCR polypeptides, which may have therapeutic uses. The altered GPCRs may also be used in vivo or in vivo in biological research. A nucleic acid encoding the altered GPCR may be used to create a transgenic animal expressing the altered GPCR may be used to create a transgenic animal expressing the altered GPCR comman G protein-coupled receptor without the need for provision of a ligand for the receptor. This is particularly useful in allowing screening of compounds against orphan receptors for which no ligand is currently known. This sequence represents CDNA encoding a human GPCR continent of the contine contined and an interest 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a constitutively active, non-endogenous version of an endogenous human G protein-coupled receptor (GPCR). The GPCR is used for screening therapeutic compounds as inverse agonists, agonists or partial agonists. The GPCR can be also be used to elucidate and understand the roles of GPCRs in normal and diseased humans. The GPCR need not be purified and isolated to be used to screen for therapeutic compounds. The utility of the GPCR as a research tool is enhanced because the role of a particular receptor can be understood before the endogenous ligand is identified. The present sequence is used in the exemplification of the present invention.
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therapeutic
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                                                                            protein-coupled receptor; GPCR;
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98US-00170496.
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Best Local Similarity 100.0%;
Matches 2724; Conservative 0
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(BEHA/) BEHAN D P.
(CHAL/) CHALMERS D T.
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                                           Human HG38 cDNA
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07-AUG-1998;
13-OCT-1998;
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New antisense oligonucleotide comprising a sequence targeted to a nucleic acid encoding G protein-coupled receptor 49, useful for preparing a composition for treating e.g., neural or endocrine system disorder.
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                                                                                                                                           TCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTTATGACCTG
TGGACAAGATCAAAACACCCAAGCTTGATGTCAATTAACTCTGATGATGTGGAAAAAACAG
                                                                      TCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTTATGACCTG
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endocrine system disorder; gene therapy; antisense therapy; human;
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                                                                                         AGCAGTATGGACGACCTTCATAAGAAAGATGCTGGAATGTTTCAGGCTCAAGATGAACGT
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Transcular disorder; metabolic disorder; nutritive disorder; cancer;

Transcular disorder; net disorder; nutritive disorder; cancer;

Transcular disorder; nerus disorder; nutritive disorder;

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The invention relates to human and mouse G protein-coupled receptors

(GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing and nucleic acids of the invention; methods of screening for associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR pene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the trasngenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising comprising a GPCR nucleic acid. The GPCR polymeticles of the invention. The invention further discloses variants of the GPCR polymeticles and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of discrets of the adrenal gland; disorders (e.g., Alzheimer's disease, (e.g., Crohn's disease including neuropathy, Parkinson's disease or schizophrenia); disorders of the adrenal gland; disorders of the colon or intestine conversion, and solution disorders of the colon or intestine conversion of an amenia or leukaemia); immuned isorders of e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders (e.g., autoimmune disorders (e.g., canders (e.g., canders (e.g., canders (e.g., canders)); muscular disorders (e.g., autoimmune disorders (e.g., canders); the present sequence represents a GPCR-encoding thyroid (e.g., canders). The present sequence represents a GPCR-encoding part did not form part of the printed sequence represents a GPCR-encoding part of the hown were obtained sequence represents directly from WIPO at the colon of the printed sequence are appeared the disorders of the electronic
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                                                                                                  Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina pectoris, Parkinson's disease.
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Pavlova MN, Vassilatis D,
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ilarity 100.0%; Pred. No. 0;
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GCTCTGACATACATTCCCAAGGGAGCATTCACTGGCCTTTACAGTCTTAAAGTTCTTATG 360

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GCTCTGACATACATTCCCAAGGGAGCATTCACTGGCCTTTACAGTCTTAAAGTTCTTATG

1411 GCATTTGGAGTGTGAGAATGCCTATAAGATTTCTAATCAATGGAATAAAGGTGACAC 1500	7 4-4 4-4 7 4-4 4-4	1801 GCAGTGAACATGCTCACGGGAGTCTCCAGTGCCGTGCTGGTGTGGATGCGTTCACT 1860	1921 GGTTTTTGFCCATTTTGCTTCAGAATCATCTGTTTTCCTGCTTACTCTGGCGCCCTG 1980	2041 CTGAAAGTAATCATTTTGCTCTGTGCCTGACCTTGACCATGGCCGCAGTTCCCCTG 2100	2161 AGCACCATGGGCTACATGGTCGCTCTTGCTCAATTCCCTTTGCTTCCTCATGATG 2220	2281 GACTGCTCTAIGGTAAAACACATTGCCCTGTTGCTCTTCACCAACTGCATCCTAAACTGC 2340 [2401 ATTAAGTTTATCCTTCTGGTGGTGGTGCCACTTCCTGCATGTCTCAATCCCCTTCTGC 2460 [
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whose expression is upregulated or downregulated in specific cancers or there diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting; colypeptide of the invention; use of such antibodies for drug targeting; colypeptides and methods are useful for diagnosing, prognoshing and treating antibodies and methods are useful for diagnosing, prognoshing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atheroscalerosis, inflammatory diseases, autoimmune diseases, ratinal neovascularistaion syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GGGGCCACCTCCCCAGGTCTGGTGTTGCTGAGGGCTGCCCCACACACTGTCATTGC 120
                                            The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTCTGACATACATTCCCAAGGGAGCATTCACTGGCCTTTACAGTCTTAAAGTTCTTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   601 ATACCAGACTATGCCTTTGGAAACCTCTCCAGCTTGGTAGTTCTACATCTCCATAACAAT
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                                                                                                                                                                                                                                                                                                                                                                                                            sequence represents a nucleic acid sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2880 BP; 710 A; 754 C; 594 G; 822 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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100.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
  SEQ ID NO C168; 1385pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 2724; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, differential expression, cancer; angiogenic disorder,
fibrotic disorder, psoriasis; ischaemia; heart disease, atherosclerosis;
inflammatory disease, autoimmune disease;
                                                                                      TCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTTATGACCTG
TCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTTATGACCTG
                                                                                                                                                             CCTCCCAGTTCCGTGCCATCACCAGCTTATCCAGTGACTGAGAGCTGCCATCTTTCCTCT
                                                                                                                                                                                  CCTCCCCAGTTCCGTGCCATCACCAGCTTATCCAGTGACTGAGAGCTGCCATCTTTCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       retinal neovascularistaton syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PA;
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E, Zlotnik /
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20010S-0340376P

20020S-034731P

20020S-0347349P

20020S-035520P

20020S-0355714P

20020S-0356717P
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2002US-0370110P.
2002US-0372246P.
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2002US-0396839P.
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2001US-0334393P.
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08-FEB-2002;
13-FEB-2002;
20-FEB-2002;
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04-APR-2002;
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This sequence encodes the human G protein-coupled receptor (GPCR) known as HG38. The HG38 protein and corresponding nucleic acid, may be used in the method of the invention for detecting colon or lung cancer. The first method involves performing an assay to determine the amount of HG38 in a sample of colon or lung tissue, and comparing the amount of protein to standard, thus detecting expression of protein in sample, where clifferential expression of protein in sample, where clifferential expression of protein in sample, where compared with the standard is diagnostic of colon or lung cancer. The second method involves hybridizing a composition compiler, to nucleic acids of a sample of colon or lung tissue under conditions to form at least one or its complement, and a labelling moiety, to nucleic acids of a sample of colon or lung tissue under conditions to form at least one comparing complex formation to a standard, where the comparison reflects differential expression of the polymclectide in the sample relative to the standard and is diagnostic of a colon or lung cancer. This first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene; human ; G protein-coupled receptor ; GPCR; HG38; colon ; lung
                                                                                                                             2581 TCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTTATGACCTG
2629 TCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTTATGACCTG
Detecting colon or lung cancer, by determining amount of protein in sample, comparing amount of protein to standard, and differential expression of protein in sample indicates colon or lung cancer.
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TTTCCTGATTTAACTGGAACTGGAACCTGGAGGGTCTGACTTTAACTGGAGGCACAGATC	1141 CTAGGARATATGAATTTAGGAATTTAAGTTGACGTGGAGTGGTTAGGTTGGCTTC 1200 1158 CTAAGACATAATGAAATTTACGAATTAAAGTTGACATTCCAGCAGTTGCTTAGCCTT 1217 1201 CGATGGCTGAATTTGGCTTGGAAAATTGCTATTATTCACCCCAATGCATTTCCACT 1260 1218 CGATGGCTGAATTTGGCTTGGAAAATTGCTATTATTCACCCCAATGCATTTTCCACT 1260 1218 CGATGGCTGAATTTGGCTTGGAAAATTGCTATTATTCACCCCAATGCATTTTCCACT 1277	1261 TIGCCATCCCTAATAAAGCTGGACCTATCGTCCAACCTCCTGTCGTCTTTTCCTATAACT 1320	1381 TCATCTGAAAACTTTCCAGAACTCAAGGTTATAGAAATGCCTTATGCTTACCAGTGCTGT 1440	AGCAGTATGGACGACCTTCATAGAAAAGATGCTGGAATGTTTCAGGCTCAAGATGAACGT	GACCTTGAGATTTCTTTCTTTTGAGGAGGAGCCTGAGAGCCTTCATTCA	1681 AGAATTGGAGTCTGGACCATAGCAGTTCTGGCACTTAATGCTTTTGGTGACTTCT 1740	1801 GCAGTGAACATGCTCACGAGAGTCTCCAGTGCCGGCTGGCT		1981 GAGCGTGGCTTCTGTGAAATATTCTGCAAAATTTGAAACGAAAGCTCCATTTTCTAGC 2040 [
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CC method enables earlier diagnosis before the patient is symptomatic. Anti- CC HG38 antibodies are useful for treating colon or lung cancer. XX SQ Sequence 2973 BP; 757 A; 759 C; 607 G; 850 T; 0 U; 0 Other; Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 2724; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Aggregator CCGGCTCCGGGCTCTGCCTGCCTGCTGCTGCTGCTGCTGC	Oy 61 GGGGCAGCTCTCCCAGGTCTGGTGTTGCTGAGGGGCTGCCCCACACAGTCATTGC 120 Db 78 GGGGCAGCTCTCCCCAGGTCTGGTGTTTGCTGAGGGGTTGCCCCACACTGTCATTGC 137 Qy 121 GAGCCCGACGCAGGATGTTGCTCAGGGGGGCTCCCGACCTGGGGGCTCTCGGAGCTG 180	181 CCTTCCAACCTCAGGATTTCCTCCTACCTAGACCTCGATATGAACAACAGGAACTGCAGGAACTAGACCTCGAACAACAACAACAACAACAACAACAACAACAACAACAA	301 GCTCTGACATACATTCCCCAGGGGGCGTTTCCTGGGCCTTTACAGTCTTAAAGTTCTTATG 318 GCTCTGACATACATTCCCCAGGGGGGGCGTTTCACTGGCCTTTACAGTCTTAAAGTTCTTATG 318 GCTCTGACATACATTCCCCAGGGGGGCCTTTACAGTCTTAAAGTTCTTATG 361 CTGCAGAATACATCAGCTAACAGCGGCCTTTACAGAATTGCGAAGTTCTTATG	378 CTGCAGAATAATCAGCTAAGACACGTAACCACAGAAATTTGCGAAGCCTT 421 CAATCCCTGCGTCTGGATGCTAACCACATCAGCTATGTGCCCCCAAGCTGTTTCAGTGGC 138 CAATCCCTGCGTCTGGATGCTAACCACATCAGCTATGTGCCCCCAAGCTGTTTCAGTGGC 438 CAATCCCTGCGTCTGGATGCTAACCACCATCAGCTATGTGCCCCCAAGCTGTTTCAGTGGC	OY 481 CIGCATTCCTGAGGCACCTGAGGTGACTAGAGGCATTAACAGAAATCCCCGTCCAG 540 bb 498 CTGCATTCCCTGAGGCACCTGTGGCTGACCATTAACAGAAATCCCCGTCCAG 557 OY 541 GCTTTAGGAGTTTATCGCAAGCCATGACCTTGCCTCAACAAAAAAAA	601 ATACCAGACTATGCCTTTGGAAACCTCTCCAGCTTGGTAGTTCTACATCTCCATAACAAT	Db 678 AGAATCCACTCCCTGGGAAAGAAATGCTTTGATGGCTCCACAGCCTAGAGACTTTAGAT 737 Qy 721 TTAAATTACAATAACTTGATGAATTCCCCACTGCAATTAGGACACTCTCCAACCTTAAA 780 Db 738 TTAAATTACAATAATCCCCACTGCCACTGCAATTAGGACACTCTCCAACCTTAAA 797 Qy 781 GAACTAGGATTTCATAGCAACAATATCAGGTCGATACCTGAGAAAGCATTTGTAGGCAAC	Db 798 GAACTAGGATTTCATAGCAACAATATCAGGTCGATAGCTGAGAAGCATTTGTAGGCAAC 857 Qy 841 CCTTCTCTTATTACAATACATTCTATGACAATCCCCATCCAATTTGTTGGAGATCTGCT 900	958 CCITCICITATIACARACARACACTACCARCCATCCARTITITICICOSASTICISCA 901 TITCAACATITACCTGAACTAAGAACACTGACTCGAATGGTGCCTCACAATTAACTGAA 918 TITCAACATTTACCTGAACTAAGAACACTGACTCTGAATGGTGCCTCACAAATAACTGAA

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whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention also relates to expression vectors and host cells comprising a nucleic acid of the invention. The invention, antibodies which specifically bind a polypeptide of the invention, use of such antibodies for drug targeting; onlypeptide of the invention, use of such antibodies for drug targeting; onlypeptides and methods are useful for diagnosing, prognosing and treating antibodies and methods are useful for diagnosing, prognosing and treating antibodies and other conditions such as psoriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, ratinal neovascularistation syndromes, scarring and utcrine fibroids. They may also be useful in wound healing and in contractine fibroids.
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Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting

Glynne R, Hevezi PA; 3, Zlotnik A;

Gish KC, Gl Wilson KE,

Ginsburg WM, 7, Watson SR,

Murray R, Aziz N,

ο, ΠΗ,

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WPI; 2003-468649/44. P-PSDB; ADN39628.

(EOSB-) EOS BIOTECHNOLOGY INC

2001US-0335394P. 2001US-0340376P. 2002US-0347349P. 2002US-0355250P. 2002US-0355250P. 2002US-0355114P.

13-NOV-2001; 21-NOV-2001; 21-NOV-2001; 20-NOV-2001; 20-NOV-2001; 20-NOV-2001; 20-NOV-2002; 20-FBB-2002; 20-FB

2002US-0368809P 2002US-0370110P. 2002US-0372246P. 2002US-0386614P

16-JUL-2002; 2002US-0396839P 22-JUL-2002; 2002US-0397775P. 09-SEP-2002; 2002US-0409450P The invention relates to nucleic acids and proteins (ADN38683-ADN40064)

Claim 8; SEQ ID NO A227; 1385pp; English. seful for diagnosing, prognosing or tinucleic acid in a biological sample.

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GAGCCCGACGGCAGGATGTTGCTCAGGGTGGACTGCTCCGACCTGGGGCTCTCGGAGCTG 380
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100.0%; Score 2724;
100.0%; Pred. No. 0;
iive 0; Mismatches
  Query Match 100.
Best Local Similarity 100.
Matches 2724; Conservative
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                                                                                           Human; differential expression; cancer; angiogenic disorder;
fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
                                                                                                                                   inflammatory disease; autoimmune disease;
retinal neovascularistaion syndrome; scarring; uterine fibroid;
detection; diagnosis; prognosis; drug screening; drug targeting;
wound healing; contraception; cytostatic; cardiant; immunomodulatory;
vulnerary; gene therapy; vaccine; gene; ss.
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260 120 320 180

Gaps

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0; Indels

DB 11; Length 3032;

sequence represents a nucleic acid sequence of the invention Sequence 3032 BP; 729 A; 816 C; 648 G; 839 T; 0 U; 0 Other; 240

381

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13-NOV-2002; 2002WO-US036810.

WO2003042661-A2

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The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
other diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
conference or absence of a pathological cell in a
conference or absence of a pathological cell in a
conference or absence of a pathological cell in a
conference or a pathological comprising a
concer and of the invention; use of such antibodies for drug targeting;
conference and methods are useful for diagnosing, prognosing and treating
cancer and other conditions such as psoriasis, ischaemia, heart disease,
atherosclerosis, inflammatory diseases, autoimmune diseases, ratinal
neovascularistaion syndromes, scarring and uterine fibroids. They may
also be useful in wound healing and in contraception. The present
                                                                                          Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
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100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                Claim 8; SEQ ID NO A130; 1385pp; English
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                             WPI; 2003-468649/44.
P-PSDB; ADN39531.
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ATCTTGTTCAATCCTCACTTTAAGGAGGATCTGGTGAGGAGCCTGAGAAAGCAAACCTACGTC
                                                                                                                                                                                                                                                                     TCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTTATGACCTG
                                                                     ATCTTGTTCAATCCTCACTTTAAGGAGGATCTGGTGAGCCTGAGAAAGCAAACCTACGTC
                                                                                                                                                       TGGACAAGATCAAAACACCCAAGCTTGATGTCAATTAACTCTGATGATGTCGAAAAACAG
                                                                                                                                                                                               TGGACAAGATCAAAACACCCCAAGCTTGATGTCAATTAACTCTGATGATGTCGAAAAACAG
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Murray R, Watson SR,
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2001US-0334393P.
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29-MAR-2002;
04-APR-2002;
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08-FEB-2002;
13-FEB-2002;
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08-JAN-2002;
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Mack DH,
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TTTCCTGATTTAACTGGAACTGCAAACCTGGAGGTCTGACTTTAACTGGAGCACAGATC 1268
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                                                                    CAATCCCTGCGTCTGGATGCTAACCACATCAGCTATGTGCCCCCCAAGCTGTTTCAGTGGC
                                                                                                                            CTGCATTCCCTGAGGCACCTGTGGTTGACAATGCGTTAACAGAAATCCCCGTCCAG
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                                                                                                                                                                    GCTTTTAGAAGTTTATCGGCATTGCAAGCCATGACCTTGGCCCTGAACAAAATACACCAC
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The invention relates to a combination comprising CDNAs that are differentially expressed in response to steroid treatment. Also included are the following: a high throughput method for using a cDNA to detect differential expression of mucleic acids in a sample; and a high throughput method of screening molecules or compounds to identify a throughput method of strandard defines a stage of that wilson disease and comparison of a strandard defines a stage of that disease. The high throughput method of screening molecules or compounds to identify a ligand that specifically binds a cDNA comprises: combining the combination with molecules or compounds under conditions to allow specific binding; and detecting specific binding between each cDNA and at least one molecule or compound. The molecules or compounds are regulatory proteins. The combination is useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirhosis or hepstitis. The present sequence represents a human cDNA which is differentially expressed in steroid-induced C3A liver cells. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO
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TCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTTATGACCTG
                                                                                                                                                                                       TCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTATGACCTG
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Query M Best Lo	Query Match 100.0%; Score 2724; DB 12; Length 4570; Best Local Similarity 100.0%; Pred. No. 0; Marches 2724. Conservative of Mismarches of Indels of Cars of	λό qα 	1021 TCATCTTCCTCAAACGTCTGCAATCAGTTACCTAATCTCCAAGTGCTAGATCTGTCT 1080
δο qα	TOGGTGTGCCCCTGCCTTGCCTGTGCTGCTGCAGTGGCGACC 60	8 &	1081 TACAACCTATTAGAAGATTTACCCAGTTTTTCAGTCTGCCAAAAGCTTCAGAAAATTGAC 1140
දු අ	61 GGGGGGAGCTCTCCCAGGTCTGGTGTTGCTGAGGGGCTCCCCCACACACTGTCATTGC 1	& 8	1141 CTAAGACATAATGAAATCTACGAAATTAAAGTTGACACTTTCCAGCAGTTGCTTAGCCTC 1200
දු දු	AGCTG 1	ጵ 8	01 CGAICGCIGAAITIGGCIIGGAACAAAAIIGCIAITAIICACCCCAAIGCAITITCCACI 126
& 8	181 CCTTCCAACCTCAGCGTCTTCACCTCCTAGACCTCAGTATGAACAACATCAGTCAG	& 4	1261 TIGCCATCCCTAATAAAGCTGGACCTATCGTCCAACCTCCTGTCGTCTTTTCCTATAACT 1320
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ò q	361 CTGCAGAATAATCAGCTAAGACACGTACCCACAGAAGCTCTGCAGAATTTGCGAAGCCTT 420 	<u>දි</u> සි	1441 GCATTTGGAGTGTGTGAGAATGCCTATAAGATTTCTAATGGATAAAGGTGACAC 1500
& 8	CAATCCCTGCGTCTGGATGCTAACCACATCAGCTATGTGCCCCCCAAGCTGTTTCAGTGGC 4	& 43	1501 AGCAGTATGGACGACCTTCATAAGAAGATGCTGGAATGTTTCAGGCTCAAGATGAACGT 1560
<i>≿</i> 8	100AG	<i>ኤ</i> 8	1561 GACCTTGAAGATTTCCTGCTTGACTTTGAGGAAGACCTGAAAGCCCTTCATTCA
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ે કે ક	AGAATCCACTCCCTGGGAAAAAATGCTTTGATGGGCTCCACAGCCTAGAGACTTTAGAT	& 93	1741 ACAGITITCAGAICCCCICTGIACAITICCCCCCAITAAACTGITAAITGGGGTCAICGCA 1800
8 & 8	TTAAATTACAATAACCTIGATGAATTCCCCACTGCAATTAGAACACTCTCCAACCTTAAA 78	S Q	GCGTTCACT 186
& 8	GAACTAGGATTICATAGCAACAATATCAGGTGGATACCTGAGAAAGCATTIGTAGGCAAC 	& 8 -	ATGTCATT 19
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8 8	TITCAACATITACCIGAACTAAGAACACTGACTCTGAATGGTGCCTCACAAATAACTGAA 96	è 8	1981 GAGCGTGGGTTCTCTGTGAAATATTCTGCAAAATTTGAAAGGAAGCTCCATTTTCTAGC 2040
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transmembrane domain 6; drug screening; agonist;
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CTGGGTGGCAGCAAGTATGGCGCCTCCCCTCTGTGCCTTTGCCTTTTGGGGGAGCCC
                                 AGCACCATGGGCTACATGGTCGCTCTCATCTTGCTCAATTCCCTTTGCTTCCTCATGATG
                                              ACCATTGCCTACACCCCAAGCTCTACTGCAATTTGGACAAGGGAGCCTGGAGAATATTTGG
                                                                                         ACCATTGCCTACACACACTCTACTGCAATTTGGACAAGGGAGACCTGGAGAATATTTGG
                                                                                                                                          GACTGCTCTATGGTAAAACACATTGCCCTGTTGCTCTTCACCAACTGCATCCTAAACTGC
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Synthetic.
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contensions trained by Comparable acceptors (GPCRs, AAY90643-AAY90677 and AAY90681-Y90687), and to DNA encoding them (AAA30709-A30743) and AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TWG). A non-endogenous amino acid, X, is substituted for an endogenous residue in IC3 at a postion 16 amino acids N-terminal of an endogenous proline in TWG to form a sequence X-C (AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this posticion is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Pro may be capagenous, non-endogenous, or a mixture of endogenous and non-endogenous cresidues. The constitutively active GPCRs are useful for identifying antagonists for a partial agonists for use as pharmaceutical agents. The mutant proteins are also useful in research settings for clucidating the roles of the receptors in normal and diseased conditions. Antagonists for a particular GPCR are used diseased conditions. Compounds without the need for endogenous ligands. Sequences AAA30799-CC Compounds without the need for endogenous ligands. Sequences AAA30799-CC CAAA30743 and AAA30773-rasory Prepresent DNAs encoding the mutant human CC GPCRs of the invention
                                                                                                                                                                                                                                                            invention relates to constitutively active, non-endogenous versions
                                                                              Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
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WPI; 2000-329165/28.
P-PSDB; AAY90687.
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Score 2720.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method for treating a non-endogenous, constitutively active version of an endogenous human G protein-coupled receptor (GFCR) that has a transmembrane-6 (TM6) region and an intracellular-3 (IC3) region, by substituting a specific amino acid in the TM6 region with a different amino acid, and testing for constitutive cutivity. The method is useful for creating a constitutively active version of an endogenous human GPCR that comprises a transmembrane for region and an intracellular loop 3 region. The altered human GPCR polypeptides are useful for screening test compounds for identification of inverse agonists or partial agonists of GPCR polypeptides, which may have therapeutic uses. The altered GPCRs may also be used in vivo or in vitro in biological research. A nucleic acid encoding the altered GPCR may be used to create a transgenic animal expressing the altered GPCR remay be used to create a transgenic animal expressing the altered GPCR. The method allows screening for compounds that modulate the activity of a human G protein-coupled receptor without the need for provision of a ligand for the receptor. This is particularly useful in allowing currently known. This sequence represents cDNA encoding a human GPCR currently known. This sequence represents cDNA encoding a human GPCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Creating a constitutively active version of an endogenous human G protein coupled receptor (GPCR) comprises substituting a specific amino acid in the transmembrane-6 region with a different amino acid, and testing for
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                                                                                                                                                                                         Human, gene; ss; G protein-coupled receptor; GPCR;
transmembrane-6 region; TM6; intracellular-3 region; IC3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.9%; Score 2720.8; ilarity 99.9%; Pred. No. 0; Conservative 0; Mismatches
                                                                                                                                                                 G protein-coupled receptor cDNA #79
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              GTGGCATTTGTCCCATGTCTCTAA
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                                                                                        ADC22796 standard; cDNA; 2724
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98US-00060188.
98US-0090783P.
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                                                                                                                                        (first entry)
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Best Local Simil
Matches 2722; (
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26-JUN-1998;
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Sequence 418,
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GenCore version 5.1.6/
Copyright (c) 1993 - 2005 Compugen Ltd.
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855-1 Sequence 1, Appli Sequence 1, Appli 434-1209 Sequence 1, Appli 564-1209 Sequence 5124, Ap 1450-16866 Sequence 5124, Ap 1450-9 Sequence 9, Appli 657B-9 Sequence 9, Appli 657B-15 Sequence 15, Appli 657B-12 Sequence 11, Appli 657B-13 Sequence 11, Appli 657B-11 Sequence 11, Appli 657B-11 Sequence 11, Appli 657B-11 Sequence 11, Appli 657B-13 Sequence 11, Appli 657B-11	NTS	us, Constitutively Activated Human G Pro	2724; DB 4; Length 2724; No. 0; natches 0; Indels 0; Gaps 0;	ATGACACCTCCCGGCTCGGTGTGCTCCTGTCCTTGCCTGTGCTGCT	GGGGGCACTCTCCCAGGTCTGGTGTTGCTGAGGGCTGCCCCACACACTGTCATTGC 120	GAGCCCGACGGCAGGATGTTGCTCAGGGTGGACTGCTCCCACCTGGGGCTCTCGGAGCTG 180 	CCTTCCAACTCCAGGGTCTTCACCTCCTAGCTCAGTATGAACAACATCAGTCAG
US-08-482- US-09-016- US-09-016- US-09-949- US-09-9461- US-09-461- US-09	ALIGNMENT	ULT 1 09-170-496D-263 equence 263, Application US/09170496D atent No. 6555339 ENERAL INFORMATION: APPLICANT: Behan, Dominic P. APPLICANT: Liaw, Chen W. TITLE OF INVENTION: No. 6555339-Endogenous, TITLE OF INVENTION: Receptors FILE REPERENCE: AREN-0040 CURRENT APPLICATION UMBER: US/09/170,496D CURRENT PILING DATE: 1998-10-13 NUMBER OF SEQ ID NOS: 294 SOFTWARE: PatentIn version 3.1 ENGTH: 2724 TYPE: DNA ORGANISM: Homo sapiens	Score Pred. ; Mis	CGGTGTGCTCCT CGGTGTGCTCCT	STCTGGTGTGTT 	STTGCTCAGGGTV 	CTTCACCTCCTA CTTCACCTCCTA
23179 23179 23179 20179		'ULT 1 '09-170-496D-263 'equence 263, Application US/09170496D 'atent No. 6555339 'ENERAL INFORMATION: APPLICANT: Behan, Dominic P. APPLICANT: Liaw, Chen W. APPLICANT: Liaw, Chen W. TITLE OF INVENTION: Receptors FILE REPRENCE: AREN-0040 CURRENT APPLICANT: 1998-10-13 NUMBER OF SEQ ID NOS: 294 SOFTWARE: PatentIn version 3.1 LENGTH: 2724 TYPE: DNA ORGANISM: Homo sapiens 09-170-496D-263	100.0%; larity 100.0%; Conservative 0		CTCTCCCAGO CTCTCCCAGO	CGCCAGGATC	CCTCAGCGT(
		1-496D-263 1e 263, Application U No. 6555339 1o. INFORMATION: NAIT: Behan, Dominic NAIT: Chalmers, Derei NAIT: Liaw, Chen W. OF INVENTION: No. 65 OF INVENTION: Recep LEFERNE: AREN-0040 IT APPLICATION UNDER IT APPLICATION UNDER IT FILING DATE: 1998 1 OF SEQ ID NOS: 294 1 RE: Patentin version NO 263 1 H: 2724 1 LISM: Homo sapiens 1 HISM: Homo sapiens 1 HISM: Homo sapiens	겉	ATGGACAC(ATGGACACC	GGGGGCAG(GGGGGCAG(GAGCCCGA(GAGCCCGAC	CCTTCCAAC
228 329 331 331 331 332 333 334 335 335 336 337 337 337 337 338 337 337 337 337 337		SULT 1 -09-170-496D-263 Sequence 263, Application Betant No. 6555339 GENERAL INFORMATION: APPLICANT: Behan, Dominic APPLICANT: Chalmers, Der APPLICANT: Liaw, Chen W. TITLE OF INVENTION: No. 6 TITLE OF INVENTION: NO. 8 TITLE OF INVENTION: 199 NUMBER OF SEQ ID NOS: 294 SOFTWARE: PALENTIN VERSION SEQ ID NO. 263 TENGTH: 2724 TYPE: DNA ORGANISM: Homo sapiens -09-170-496D-263	Match Local	п п	. 61	121	181
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GCTCTGACATACATTCCCAAGGGAGCATTCACTGGCCTTTACAGTCTTAAAGTTCTTATG 360

CTGCAGAATAATCAGCTAAGACACGTACCCACAGAAGCTCTGCAGAATTTGCGAAGCCTT

GCTCTGACATACATTCCCAAGGGAGCATTCACTGGCCTTTACAGTCTTAAAGTTCTTATG

Comparison Com	OY 421 CAATCCCTGCGTCTGGATGCTAACCACATCAGCTATGTGCCCCCAAGCTGTTTCAGTGGC 480	OY 481 CTGCATTCCCTGAGGCACCTGTGGCTGGATGACAATGCGTTAACAGAAATCCCCGTCCAG 540	OY 541 GCTTTTAGAAGTTTATCGGCATTGCAAGCCATGACCTTGGCCCTGAACAAAATACACCAC 600	OY 601 ATACCAGACTATGCTTTTGGAAACCTCCAGGCTTGGTAGTTCTACATCTCCATAACAAT 660	OY 661 AGAATCCACTCCCTGGGAAAGAATGCTTTGATGGGCTCCACAGCCTAGAGACTTTAGAT 720	OY 721 TTAAATTACAATAACCTIGATGAATTCCCCACTGCAATTAGGACACTCTCCAACCTTAAA 780	OY 781 GAACTAGGATTTCATAGCAACAATATCAGGTCGATACCTGAGAAAGCATTTGTAGGCAAC 840	OY 841 CCTTCTTATTACAATACATTCTATGACAATCCCATCCAATTTGTTGGGGGATCTGCT 900	OY 901 TITCAACAITTACCTGAACTAAGAACACTGAATGGTGCCTCACAAATAACTGAA 960	OY 961 TITCCTGAITTAACTGGAACTGCAAACCTGGAAGTCTGACTTTAACTGGAGCACAGATC 1020	1021 TCATCTTCCTCAAACCGTCTGCAATCACTTACCTAATCTCCAAGTGCTAGATCTGTCT 	Oy 1081 TACAACCTATTAGAAGATTTACCCAGTTTTTCAGTCTGCCAAACCTTCAGAAATTGAC 1140	1141 CTAAGACATAATGAAATCTACGAAATTAAAGTTGACACTTTCCAGCAGTTGCTTAGCCTC 1402 CTAAGACATAATGAAATTAAAGTTGACACTTTCCAGCAGTTGCTTAGCCTC	1201 CGATCGCTGAATTTGGCTTGGAACAAATTGCTATTATTCACCCCAATGCATTTTCCACT 126 1462 CGATCGCTGAATTTGGCATTGGAACAAAATTGCTATTATTCACCCCAATGCATTTTCCACT 1501 CGATCGCTGAATTTGGCTTGGAACAAAATTGCTATTATTCACCCCAATGCTTTTCCACT 1501 CGATCGCTGAATTTTCACTCCAAAATTGCTATTATTCACCCCAATGCTTTTCCACT 1501 CGATCGCTGAATGCTTATTCACTCCAATGCTTTTTCACTCCAATGCTTTTTCAATGCTTTTTCAATGCTTTTTTCAATGCTTTTTTTT	1261 TIGCCATCCCTAATAAGCTGGACCTATCGFCCACCTCTGTGTGTGTTTTCCTATAGCT 1522 TIGCCATCCCTAATAAGCTGGACCTATCGTCCACCTCTGTCGTCTTTTCCTATAACT 1521 ACCOUNTAATAAGCTGGACCTATCGTCCAACCTCTGTCGTCTTTTCCTATAACT	1581 GGGTTACATGGTTTAACTCACTTAAAATTAACAGGAAATCATGCCTTACAGAGCTTGATA 1582 GGGTTACATGTTTAACTCACTTAAAATTAACAGGAAATCATGCCTTACAGAGCTTGATA	OY 1381 TCATCTGAAACTTTCCAAAGTTATAGAAATGCCTATGCTTACCAGTCCTG 1440 Db 1642 TCATCTGAAACTTTCCAGAACTCAAGGTTATAGAAATGCCTTATGCTTACCAGGTGCTG 1701	QY 1441 GCATTGGAGTGTGGAGAATGCCTATAAGATTCTAATCAATGGAATAAAGGTGACAAC 1500 1102 GCATTTGAGGTGTGTGAGAATGCCTATAAGATTTCTAATCAATGGAATAAAGGTGACAAC 1500 1702 GCATTTGGAGTGTGTGAGAATGCCTATAAGATTTCTAATCAATGAGATAAAGGTGACAAC 1761 09 1501 AGCAGTATGGACGTCCATAAGAAGATGCTTCATAAGAAGATGCTTCAAAGATGCTTCAAAGATGCTTCAAAGATGCTTCAAAGATGCTTCAAGATGAAGATGCTTCAAAGATGCTTCAAAGATGCTTCAAAGATGCTTCAAAGATGCTTCAAAAGATGCTTCAAAAAGATGCTTCAAAAAGATGCTTCAAAAAGATGCTTCAAAAAGATGCTTCAAAAAGATGCTTCAAAAAAAGATGCTTCAAAAAAAA
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APPLICANT: Ghosh, Reena
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6783969el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
SOFTWARE DE FL.genes Version 2.0
SEQ ID NO 723
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Patent No. 6783969
GENERAL INFORMATION:
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Yamazaki, Victoria
Chen, Rui-hong
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APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Uinod
APPLICANT: Ren, Feiyan
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Xue, Aidong J.
Zhao, Qing A.
Wang, Jian-Rui
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Matches 1116; Conservative
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Ghosh, Reena
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ORGANISM: Homo sapiens
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; LOCATION: (1)
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APPLICANT: Roopa, Reddy
APPLICANT: Guegler, Karl, J.

FILE REPERENCE: PA-013 US
CURRENT APPLICATION NUMBER: US/09/495, 050A
CURRENT APPLICATION NUMBER: 60/118, 318
PRIOR PILING DATE: February 1, 1999
NUMBER OF SEQ ID NOS: 305
SOFTHARE: PERL PROGram
SEQ ID NO 220
LENGTH: 723
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; OTHER INFORMATION: Incyte ID No. 6492505 2603450CT1
US-09-495-050A-220
                                                                              Sequence 220, Application US/09495050A Patent No. 6492505 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 99.7
Matches 722; Conservative
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ORGANISM: Homo sapiens
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Sequence 214, Application US/09495050A

Batent No. 6492505

GENERAL INFORMATION:
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GENERAL INFORMATION:
GREGICANT: Roopa, Reddy
APPLICANT: ROOPA; Reddy
APPLICANT: AL'YOUNG, Janice
TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED FILE REFERENCE: PA-0013 US
CURRENT APPLICATION NUMBER: 2000-01-31
PRIOR PLING DATE: 2000-01-31
PRIOR FILING DATE: February 1, 1999
NUMBER OF SEQ ID NOS: 305
SOFTWARE: PERL PROGram
SEQ ID NO 214
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; OTHER INFORMATION: Incyte ID No. 6492505 2470285CT1
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Patent No. 5888716
GENERAL INFORMATION:
APPLICANT: ELSHOURBAGY, NABIL A
APPLICANT: LI, XIAOTONG
APPLICANT: LI, XIAOTONG
TITLE OF INVENTION: NOVEL 7TM REC)
ITILE OF INVENTION: NOVEL 7TM REC)
CORRESPONDENCES: A
ADDRESSE: RATHER & PRESTIA
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                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: PERESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,757
FILING DATE: 30-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEPAX: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4203 base pairs
                                                                                                                                                                                       3: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 54.9
Matches 1090; Conservative
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-866-757-1
                                                                                                                       ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
. P.O. BOX 9
VALLEY FORGE
                                                                                                                                                                                                                 COMPUTER: IBM Con
OPERATING SYSTEM:
                                                      PA
USA
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Pred. No. 2.2e-146;
); Mismatches 863;
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APPLICANT: BERGSMA, DERK J
TITLE OF INVENTION: NOVEL 7TM RECEPTOR (H2CAA71)
FILE REFERENCE: GH-70055-1
CURRENT APPLICATION NUMBER: US/09/153,593A
CURRENT APPLICATION NUMBER: 1980-09-15
EARLIER FILING DATE: 1997-09-15
SEALIER FILING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 4
SOFTWARE FRAEKSEQ for Windows Version 3.0
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APPLICANT: ELSHOURBAGY, NABIL A
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Best Local Similarity 54.9%;
Matches 1090; Conservative C
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  GGGGTTGGTTGCCATGTCATTGGTTTTTTTGTCCATTTTTTGCTTTCAGAATCATCTGTTTTTC
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APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
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CURRENT APPLICATION NUMBER: US/09/482,273

CURRENT PILING DATE: 2000-01-13

EARLIER PELICATION NUMBER: PCT/US99/15849

EARLIER PILING DATE: 1999-07-14

EARLIER APPLICATION NUMBER: 60/092,921

EARLIER APPLICATION NUMBER: 60/092,922

EARLIER APPLICATION NUMBER: 60/092,926

EARLIER APPLICATION NUMBER: 60/092,926

EARLIER PILING DATE: 1998-07-15

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ORGANISM: Homo
US-09-482-273-75
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LENGTH: 2703
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4.6%; Score 125.8; DB 4; Length 2703;

Query Match

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                                                                           Indels
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APPLICANT: ELSHOURBAGY, NABIL A
APPLICANT: LI, XIAOTONG
APPLICANT: LI, XIAOTONG
APPLICANT: BERGSMA, DERK J
TITLE OF INVENTION: NOVEL 7TM RECEPTOR (H2CAA71)
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAINER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
                              Pred. No. 2.1e-27;
); Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COREATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,757
FILING DATE: 30-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/866,757
FILING APPLICATION DATA:
APPLICATION NUMBER: STILL OF THE STILL OF 
59.3%; Pre.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08866757 Patent No. 5858716
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nucleic acid
                         Best Local Similarity 59.3
Matches 214; Conservative
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US-08-866-757-3
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2443 CTCAATCCCCTTCTCTACATCTTCAATCCTCACTTTAAGGAGGATCTGGTGAGCCTG 2502
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2408 ITATCCTTCTGGTGGTAGTCCCACTTCCTGCATGTCTCCAATCCCCTTCTCTACATCTTGT
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                                              2348 CTTTCTTGTCCTTCTCCTCTTTAATAAACCTTACAFTTATCAGTCCTGAAGTAATTAAGT
                                                                                           200 ceririricarirecaccaricarcacaarcreraricaeccccaaaraarear
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Pred. No. 3.4e-24;
0; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 101, Application US/09482273
Factence 101, Application US/09482273
Factence 101, Application US/09482273
Factence 101, Sequence 101, Application US/09482273
GENERAL INFORMATION:
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: PZ030P1
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 1000-01-13
EARLIER FILING DATE: 1999-07-14
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER PLICATION NUMBER: 60/092,922
EARLIER PLICATION NUMBER: 60/092,956
EARLIER FILING DATE: 1998-07-15
SOFTWARE: PATENTING DATE: 1998-07-15
SOFTWARE: PATENTING DATE: 1998-07-15
SOFTWARE: PATENTING DATE: 1998-07-15
INDUBER OF SEQ ID NOS: 267
SOFTWARE: PATENTIN VOR: 2.0
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Best Local Similarity 59.3%;
Matches 214; Conservative 0
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; ORGANISM: Homo sapiens
US-09-482-273-101
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                                                                                                                           Length 473;
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                                                                                                                      4.5%; Score 123.8; DB 2; Length 61.2%; Pred. No. 2.2e-27; tive 0; Mismatches 127; Indels
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GENERAL NO. 517-527-7

APPLICANT: ELSHOURBAGY, NABIL A

APPLICANT: ELL, XIAOTONG

APPLICANT: BERGSMA, DERK J

TITLE OF INVENTION: NOVEL 7TM RECEPTOR (H2CAA71)

FILE REFERENCE: GH-70055-1

CURRENT PAPLICATION NUMBER: US/09/153,593A

CURRENT PILING DATE: 1998-09-15

EARLIER APPLICATION NUMBER: 08/866,757

EARLIER PILING DATE: 1997-05-30

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCAATCCTCACTTTAAGGAGGATCTGG 2494
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; LOCATION: (397) (400) (406) (432) (459)
US-09-153-593-3
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Patent No. 6174994
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Matches 200; Conservative
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    STRANDEDNESS: single
TOPOLOGY: linear
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                      TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-866-757-3
                                                                                                                                               Similarity
                                                                                                                                                 Best Local Simu
Matches 200;
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POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTOR AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
1916 TCATTGGTTTTTTTTTTTTTTTTCCTTTCAGAATCATCTGTTTTCCTGCTTACTCTGGCAG 1975
                                        CGGCTGGTTTCTTCACTGTCTTTGCAAGCGAGTTATCGGTGTATACGCTGACGGTCATCA 1616
                                                                                                                            1617 CCCTGGAGCGCTGGTATGCCATCACCTTCGCCATGGCCCTGGACCGGAAGATCCGCCTCA 1676
                                                                                                                                                                                                                   1797 CCCCTCTTGCTCTGGCATATATTGTTTTTGTTCTGACGCTCAACATAGTTGCCTTCGTCA 1856
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                                                                                                                                                                                                                                                              CCCTGCTGGGTGGCAGCAAGTATGGCGCCTCCCCTCTCTGCCTTTTGCCTTTTTGGGG
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                                                                                                                                                                                                                                                                                                                                                  2156 AGCCCAGCACCATGGGCTACATGGTCGCTCTCTTGCTCAATTCCCTTTGCTTCCTCA
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                                                                                 CCCTGGAGCGTGGGTTCTCTGTGAAATATTCTGCAAAATTTTGAAACGAAAGCTCCATTTT
                                                                                                                                                                       CTAGCCTGAAAGTAATCATTTTGCTCTGTGCCCTGCCTTGACCATGGCCGCAGTTC
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/741,453A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: CUSHMAN DARBY & CUSHMAN 1615 L STREET, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 62, Application US/07741453A Patent No. 6228597 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: PARMENTIER, MARC APPLICANT: IDERT, FREDERIC APPLICANT: DUMONT, JACQUES APPLICANT: VASSART, GILBERT TITLE OF INVENTION: POLYPEPTII TITLE OF INVENTION: ACTIVITY, TITLE OF INVENTION: AND POLYPEN NUMBER OF SEQUENCES: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WASHINGTON, D.C
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COMPUTER READABLE FORM:
MEDIUM TYPE: Disk
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                                                                                                                                                                       THE DETECTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.2
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 487;
                                                                                                                        APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETI
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
CORRESPONDENCE: 1490
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 PORTER DRIVE CITY: PALO ALTO CITY: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PA-0002 US
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APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
                                                          Sequence 1469, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PA-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1469:
SEQUENCE CHARACTERISTICS:
LENGTH: 2413 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
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APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Zeller, Karen J. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 45.0
Matches 399; Conservative
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US-09-016-434-1469
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                                                                                                                                                                                                 Length 3710;
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                                                                                                                                                                                                 Score 100.2; DB 3
Pred. No. 2.2e-19;
TELECOMMUNICATION INFORMATION:
TELERAX: (202) 861-3000
TELERAX: (202) 862-0944
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTER SITICS:
LENGTH: 3710 base pairs
TYPE: NUCLEEC ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                 Query Match 3.7%;
Best Local Similarity 45.3%;
                                                                                                                                                                                                                                 Matches 403; Conservative
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Sequence 57, Application US/07741453A

Sequence 57, Application US/07741453A

Patent No. 6228597

GENERAL INFORMATION:
APPLICANT: PARMENTIER, MARC
APPLICANT: DUMONT, JACQUES
APPLICANT: DUMONT, JACQUES
APPLICANT: OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
TITLE OF INVENTION: ADD POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSE: CUSHMAN DARBY & CUSHMAN
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SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/741,453A
FILING DATE: 19911015
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST
TELEPHONINICATION INFORMATION:
TELEPHONINE: (202) 861-3000
TELEPHONE: (202) 861-3000
TELEPHONE: (202) 861-3000
TELERAX: (202) 822-0944
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COMPUTER: IBM PC compatible
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2: /cgn2_6/ptodata/2/pubpna/RPGT MEW PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 263, App	Sequence 421, App	Sequence 4, Appli	Sequence 21, Appl	Sequence 1114, Ap	Sequence 157, App	Sequence 48, Appl
SCHAME	,	US-10-251-385-263	US-10-225-567A-421	US-10-174-456-4	US-10-751-736-21	US-10-295-027-1114	US-10-482-029-157	US-10-651-237-48
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21	17	15	21	17	11	11	21	17	10	18	10	18	10	18	14	11	10	18	20	21	10	15	11	20	11	14	15	19	21	21	15	21	11	18	14	10
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100.0	100.0	6.66	8.66	94.2	94.2	94.2	76.2	36.6	30.9	30.9	30.9	30.9	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.3	29.3	28.5	28.5	28.5	28.4	26.1	24.3	24.1	24.1	23.8	22.8	22.8	20.4	20.3	20.1
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ALIGNMENTS

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Generation No. US20030105292A1

GENERAL INFORMATION:

APPLICANT: Chalmers, Derek T.

APPLICANT: Chalmers, Derek T.

APPLICANT: Chalmers, Derek T.

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: US/10/251,385

CURRENT APPLICATION NUMBER: US/10/251,385

CURRENT APPLICATION NUMBER: US/09/170,496

PRIOR APPLICATION NUMBER: US/09/170,496

PRIOR APPLICATION NUMBER: US/09/170,496

PRIOR PRIOR OF SEQ ID NOS: 294

SOFTWARE: Patentin version 3.1

SEQ ID NO 263

LENGTH: 2724
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100.0%; Score 2724;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2724; Conservative 0; Mismatches
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US-10-251-385-263
RESULT 1
US-10-251-385-263
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APPLICANT: Afar, Daniel
APPLICANT: Gisberg, Wendy M.
APPLICANT: Gisberg, Wendy M.
APPLICANT: Glyne, Richard
APPLICANT: Glyne, Richard
APPLICANT: Glyne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: March Bos bisechnology, Inc.
APPLICANT: Wateon, Susan R.
APPLICANT: Wateon, Susan R.
APPLICANT: Bos bisechnology, Inc.
APPLICANT: Wateon, Susan R.
APPLICANT: Bos bisechnology, Inc.
TITLE OF INVENTION: Methods of Exceening for Modulators of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: Methods of Sold-11-13
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-29
PRIOR PILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR PILING DATE: 2002-01-10
PRIOR FILING DATE: 2002-01-10
PRIOR PRIOR FILING DATE: 2002-01-1
2581 TCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTTATAAACCTG
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                                                                                                                                                                                                                     GTGGCATTTGTCCCATGTCTCTAA 2724
                                                                                                                                                                                                                                                                                                                                                          Sequence 1114, Application US/10295027; Publication No. US20030232350A1; GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-10-295-027-1114
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                                                                                                                                                                                                                                                                                                                     2041 CTGAAAGTAATCATTTTGCTCTGTGCCCTGCTGGCCTTGACCATGGCCGCAGTTCCCTG
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Publication No. US20050037445A1
GENERAL INFORMATION:
APPLICANT: ODIN medical A/S
TITLE OF INVENTION: Oncology drug innovation
FILE REPERENCE: P 573 PC00
CURRENT APPLICATION NUMBER: US/10/482,029
CURRENT PILING DATE: 2003-12-29
NUMBER OF SEQ ID NOS: 437
SOFTWARE: PatentIn version 3.1
SEQ ID NO 157
LENGTH: 2880
TYPE: DNA
TYPE: DNA
CREANISM: Homo sapiens
US-10-482-029-157
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Best Local Similarity 100.0%;
Matches 2724; Conservative 0
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US-10-482-029-157
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Sequence 48, Application US/10782413
Fublication No. US20050048526A1
GENERAL INFORMATION:
APPLICANT: Ortho-Clinical Diagnostics, Inc.
APPLICANT: Wang, Yixin
TITLE OF INVENTION: Colorectal Cancer Prognostics
FILE REPRENCE: VDX-5002 CIP
CURRENT APPLICATION NUMBER: US/10/782,413
CURRENT FILING DATE: 2004-02-18
FRIOR FILING DATE: 2003-08-28
NUMBER OF SEQ ID NOS: 94
SOFTWARE: PatentIn version 3.1
SEQ ID NO 48
LENGTH: 2880
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2724; Conservative 0; Mismatches
                                                                                  GIGGCATITGICCCATGICTCIAA 2724
                                                                                               TYPE: DNA
ORGANISM: human
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APPLICANT: Afar, Daniel
APPLICANT: Afar, Daniel
APPLICANT: Ginberg, Wendy M.
APPLICANT: Ginberg, Wendy M.
APPLICANT: Ginberg, Wendy M.
APPLICANT: Ginberg, Wendy M.
APPLICANT: Hevezi, Peter
APPLICANT: Hevezi, Peter
APPLICANT: Hevezi, Peter
APPLICANT: Mack, David H.
APPLICANT: Mack, Bavid H.
APPLICANT: Mack, Bavid H.
APPLICANT: Mack, Bavid H.
APPLICANT: Mack, Bos Bistechnology, Inc.
APPLICANT: Meson, Susan R.
APPLICANT: Meson, Susan R.
APPLICANT: Methods of Diagnosis of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: Whenes: US 60/35, 733
PRICK FILING DATE: 2001-11-13
PRICK PILING DATE: 2001-11-15
PRICK PILING DATE: 2001-11-15
PRICK PILING DATE: 2001-11-15
PRICK PILING DATE: 2001-11-13
PRICK PILING DATE: 2001-11-14
PRICK PILING DATE: 2002-01-16
PRICK PILING DATE: 2002-01-10
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100.0%; Score 2724;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2724; Conservative 0; Mismatches
       2749 GIGGCALTIGICCCAIGICTCTAA 2772
                                                                                                                         ; Sequence 848, Application US/10295027; Publication No. US20030232350A1; GENERAL INFORMATION:
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APPLICANT: Matray, Richard H.
APPLICANT: Matray, Richard H.
APPLICANT: Watson, Susan R.
APPLICANT: Experiment of the control o
                     2461 ATCTTGTTCAATCCTCACTTTAAGGAGGATCTGGTGAGCCTGAGAAGCAAACCTACGTC
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Pred. No. 0;
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Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Afar, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Reichard;
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
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ORGANISM: Homo sapiens
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US-10-505-486-205

Squence 205, Application US/10505486

Publication No. US20050118639A1

GENERAL INFORMATION:

APPLICANT: Takeda Chemical Industries, Ltd.

TILE OF INVENTION: Determination of a ligand FILE REFERENCE: PO3-0006FCT

CURRENT APPLICATION NUMBER: US/10/505,486

CURRENT FILING DATE: 2004-08-20

PRIOR FILING DATE: 2002-02-22

PRIOR APPLICATION NUMBER: JP 2002-45728

PRIOR FILING DATE: 2002-07-33

PRIOR APPLICATION NUMBER: JP 2002-213949

PRIOR FILING DATE: 2002-07-23

SEQ ID NO 205

LENGTH: 3438
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1261 TTGCCATCCTAATAAAGCTGGACCTATCGTCCAACCTCCTGTCGTCTTTTCCTATAACT 1320 1261 TTGCCATCCCTAATAAAGCTGGACCTATCGTCCAACCTCCTGTCGTCTTTTCCTATAACT 1320 1321 GGGTTACATGGTTTAACTCTCTCACACCTCCTGTCGTCTTTTCCTATAACT 1320 1321 GGGTTACATGGTTTAACTCACTTAAACTCACTGATA 1380 1381 TCATCTGAAAACTTTCCAGAACTTAACAGCAATCATGCCTTACAGGCTTGATA 1380 1411	1681 AGAATTGGAGTGTGGACCATAGCAGTACTTGTAATGCTTTGGTGACTTCA 1740	2041 CTGAAGTAATCATTTAGTCTGTGCCTGGCCTTGACCATGCCGCAGTTCCCCTG 2100 2101 CTGGGTGGCAAGTATGCGCCTCCCTCTGCCTGCCTTTGCCTTTTGGGAAGCCC 2160 2101 CTGGGTGGCAAGTATGGCGCTCCCTCTTGCCTTTTGGGAAGCCC 2160 2101 CTGGGTGGCAAGTATGGCGCTCCCTCTTGCCTTTTGGGAAGCCC 2160 2161 AGCACCATGGGCAAGTATGGCCTCATCTTGCTTTTGGTATG 2220 2161 AGCACCATGGGTAACACCAGCTCTACTGCTCAATTTGGTAATTTGGTAATTTTGGTAATTTTGGTAATTTTGGTAATTTTGGTAATTTTGGTAATTTTGGTAATTTTGGTAATTTTGGTAATTTTGGTAATTTTGGTAATTTTGGTAATTTTTGGTAATTTTGGTAATTTTGGTAATTTTGGTAATTTTGGTAATTTTGGTAATTTTGGTAATTTTTGGTAATTTTGGTAATTTTGGTAATTTTGGTAATTTTGGTAATTTTGGTAATTTTGGTAATTTTTGTATTTTTT

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AGAATCCACTCCCTGGGAAAGAAATGCTTTGATGGGCTCCACAGCCTAGAGACTTTAGAT 720
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR PLICATION NUMBER: US 60/334,393
PRIOR PLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-11-29
PRIOR PLING DATE: 2001-12-14
PRIOR PLICATION NUMBER: US 60/347,211
PRIOR PLICATION NUMBER: US 60/347,211
PRIOR PLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-08
PRIOR PLING DATE: 2002-01-10
PRIOR PLING DATE: 2002-01-10
PRIOR PLING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR APPLICATION NUMBER: US 60/356,714
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PRIOR FILING DATE: 2002-02-08
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Best Local Similarity 97.4%;
Matches 2648; Conservative
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US-10-295-027-1113
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DUBLICATION OF US20030232350A1
Sequence 1113, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Afar, Daniel
APPLICANT: Glynne, Richard
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APPLICANT: Hever, Peter A.
APPLICANT: Hever, David H.
APPLICANT: Watron, Suann R.
APPLICANT: Watron, Suann R.
APPLICANT: Watron, Suann R.
APPLICANT: Watron, Suann R.
APPLICANT: Watron, Sucherdenology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT APPLICATION NUMBER: US/10/295,027
FILE REFERENCE: O18501-012500US
CURRENT APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR PLING DATE: 2001-11-13
PRIOR PLING DATE: 2001-11-15
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AGAATCCACTCCCTGGGAAAGAAATGCTTTGATGGGGCTCCACAGCCTAGAGACTTTAGAT TTAAATTACAATAACTTGATGAATTCCCCACTGCAATTAGGACACTCTCCAACCTTAAA	TTAAATTACAATAACCTIGATGAATTCCCCACTGCAATTAGGACACTCTCCAACCTTAAA 7 GAACTAGGATTTCATAGCAACAATATCAGGTCGATACCTGAGAAAGCATTTGTAGGCAAC 8 	781 GAAC 784 841 CCTTCTCTTATACAATACATTCTATGACAATCCCATCCAATTTGTTGGGAGATCTGCT 900 785TACATTTCTATGACAATCCCATCCAATTCTTGGGAGATCTGCT 828	TTTCAACATTTACCTGAACTAGAACACTGACTCTGAATGGTGCCTCACAAATAACTGAA 96	TITCCTGAITTAACTGGAACTGCAAACCTGGAGAGTCTGACTTTAACTGGAGCACAGATC	4 o	- 0	CTAAGACATAATGAAATCTAGGAAATTAAGTTGACACTTTCCAGGAGTTGCTTAGCCTC 120	CGATCGCTGAATTTGGCTTGGAACAAAATTGCTATTATTCACCCCGAATGCATTTTCCACT 126	TIGGATCCCTAATAAGCTGGACTATCGTCCACCTCCTGTCGTCTTTCCTATAACT	1321 GGGTTACATGGTTTAACTCACTTAAAATTAACAGGAAATCATGCCTTACAGAGCTTGATA 1380 	TCATCTGAAAACTTTCCAGAACTCAAGGTTATAGAAATGCCTTATGCTTACCAGTGCTGT			1561 GACCTIGAAGAITICCTGCTIGAGAAGACCTGAAAGCCCTTCAITCAGTGCAG 1620 	1 IGTTCACCTTCCCCAGGCCCCTTCAAACCCTGTGAACACCTGCTTGATGGCTGGC	1681 AGAATTGGAGTGTGGACCATAGCAGTTTGGGACTTGTAATGCTTTGGTGACTTCA 1740 1609 AGAATTGGAGTGTGGACCATAGCAGTTTCTGGCACTTCATAGTTGGTGACTTCA 1668 1741 ACAGTTTTCAGAGTGCCCTCTGTACATTTCCCCCATTAAACTGTTAATTGGGGTCATCGCA 1800 1669 ACAGTTTTCAGATCCCTCTGTACATTTCCCCCATTAAACTGTTAATTGGGGTCATCGCA 1800 1669 ACAGTTTTCAGATCCCTCTGTACATTTCCCCCATTAAACTGTTAATTGGGGTCATCGCA 1728

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APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian
TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian
TITLE OF INVENTION: Cancer
CURRENT APPLICATION NUMBER: US 60/299,234
PRIOR APPLICATION NUMBER: US 60/299,234
PRIOR APPLICATION NUMBER: US 60/399,234
PRIOR APPLICATION NUMBER: US 60/315,287
PRIOR APPLICATION NUMBER: US 60/315,287
PRIOR PILING DATE: 2001-06-18
PRIOR PILING DATE: 2001-06-12
PRIOR PILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-12
PRIOR PILING DATE: 2001-14-12
PRIOR PILING DATE: 2001-16-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGCAGAATAATCAGCTAAGACACGTACCCACAGAAGCTCTGCAGAATTTGCGAAGCCTT
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 97.4%;
Matches 2648; Conservative
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ORGANISM: Homo sapiens
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1368

& 43	1801	GCAGTGAACATGCTCCACGGGAGTCTCCAGTGCCGTGCTGGCTG
ð i	1861	α .
qq	1789	TTTGGCAGCTTTGCACGACATGGTGCCTGGTGGGAATGGGGTTGGTT
· 상 원	1921	GGTTTTTTGTCCATTTTTGCTTCAGAATCATCTGTTTTCCTGCTTACTCTGGCAGCCCTG 1980
ò	1981	GAGCGTGGGTTCTCTGTGAAATATTCTGCAAATTTGAAACGAAAGCTCCATTTTCTAGC 2040
ΩÞ	1909	
ò	2041	CTGAAAGTAATTCATTTTGCTCTGTGCCCTGCTGGCCCTTGACCATGGCCGCGGTTCCCCTG 2100
Ωp	1969	CTGAAAGTAATCATTTTGCTCTGTGCCCTGCTGCCTTGACCATGGCCGCAGTTCCCCTG 2028
ò	2101	CTGGGTGGCAGCAAGTATGGCGCTCCCCTCTGCCTGCCTTTTGCCTTTTGGGAGCCC 2160
QΩ	2029	CTGGGTGGCAGCAAGTATGGCGCCTCCCCTCTCTCCCTTTTGCCTTTTGGGGAGCCC 2088
ò	2161	AGCACCATGGGCTACATGGTCGCTCTTGCTCAATTCCCTTTGCTTCCTCATGATG 2220
QQ	2089	AGCACCATGGGCTACATGGTCGCTCTCATTTCCCTTTGCTTCCTCATGATG 2148
ò	2221	ACCATTGCCTACACCAAGCTCTACTGCAATTTGGACAAGGGGACCTGGAGAATATTTGG 2280
QQ	2149	ACCATTGCCTACACCAAGCTCTACTGCAATTTGGACAAGGGAGACCTGGAGAATATTTGG 2208
'n	2281	GACTGCTCTATGGTAAAACACATTGCCCTGTTGCTCTTCACCAACTGCATCGTAACTGC 2340
QQ	2209	GACTGCTCTATGGTAAAACACATTGCCCTGTTGCTCTTCACCAACTGCATCCTAAACTGC 2268
ķ	2341	CCTGTGGCTTTCTTCTCCTCTTTAATAAACCTTACATTTATCAGTCCTGAAGTA 2400
qq	2269	CCTGTGGCTTTCTTGTCCTTCTTCTTTAATAAACCTTACATTTATCAGTCCTGAAGTA 2328
ò	2401	ATTAAGTTTATCCTTCTGGTGGTAGTCCCACTTCCTGCATGTCTCAATCCCCTTCTCTAC 2460
qq	2329	ATTAAGTITTAICCTICIGGIGGIAGICCCACTICCIGCAIGICICCAAICCCCTICICIAC 2388
ò	2461	AICTIGITCAAICCTCACTITAAGGAGGATCTGGTGAGCTGAGAAAGGAAACCTACGTC 2520
ДQ	2389	Arctigitcaaiccicactitaaagaagaicigaigaagccigaaaaagaaaacciacgic 2448
ò	2521	TGGACAAGATCAAAACACCCCAAGCTTGATGTCAATTAACTCTGATGATGTCGAAAAAAGG 2580
qq	2449	TGGACAAGATCAAAACACCCAAGCTTGATGTCAATTAACTCTGATGTGTGGAAAAACAG 2508
ò	2581	TCCTGTGACTCAACTCTAGCTTAGCTTTACCAGCTCCAGCATCACTTATGACCTG 2640
Db	2509	TCCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCATCACTTATGACCTG 2568
λ̈́o	2641	CCTCCCAGTTCCGTGCCATCACCAGGCTTATCCAGTGACTGAGAGCTGCCATCTTTCCTCT 2700
OP	2569	CCTCCCAGTTCCGTGCCATCACCAGCTTATCCAGTGACTGAGAGCTGCCATCTTTCCTCT 2628
ò	2701	GIGGCATITGTCCCATGTCT 2720
Db	2629	GIGGCATTIGICCCATGICT 2648

Search completed: July 12, 2005, 21:05:45 Job time : 1831.02 secs

Perfect score:

Sequence:

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OM nucleic

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Scoring table:

Minimum DB Maximum DB

Database

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2724 bp DNA linear GSS 16-DEC-2003
Homo sapiens GPR49 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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B1989071 4024-89 M
BB613285 BB613285
AK016357 MUB mUBCU
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BI521415 603063185
BY126232 BY126322
BY126329 BY718968
AK033699 MNB mUBCU
BB642290 BB642290
CF176392 BO0469 MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotta, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. [Lase, 2724]
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Reritera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, White, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGGACACCTCCCGGCTCGGGCTCCTGTCCTTGCCTGTGCTGCTGCAGCTGGCGACC
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Best Local Similarity 97.4%; Pred. No. 0;
Matches 2652; Conservative 0; Mismatches
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BI906257
BY126232
BY718968
AK033699
BB642290
CF176392
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/locus_tag="HCM4322"
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/gene="GPR49"
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Mus musculus GPR49 gene, VIRTUAL TRANSCRIPT, partial sequence,
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Reriaera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                          /tissue type="NEUROBLASTOMA COT 50-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                           http://www.genoscope.cns.fr/cdna?s=CSODD008DC11QP1&c=7021.f.
Location/Qualifiers
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Pred. No. 8e-290;
1; Mismatches 18; Indels 2
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/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="CSODDO08YF22"
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Best Local Similarity 95.4%; Pre
Matches 1052; Conservative 31;
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1 (Bases I to 1104)

1 (Bases I to 1104)

1 (Bases I to 1104)

Full-length cDNA libraries and normalization
Unpublished (2001)

On Feb 13, 2001 this sequence version replaced gi:31068631.

Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EWRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODEGOTYC19"
/tissue type="FLACENTA"
/clone="Taxon:pcMVSPORT 6; lst strand cDNA was primed
with a Not1-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Genoscope Control of Sequences Contact: Genoscope - Centre National de Sequences Centre Centre National de Sequences Centre Caston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: Seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr email: seqref@genoscope.cns.fr end of NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a
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                                                                                        AACTGTTAATTGGGGTCATCGCAGCAGTGAACATGCTCACGGGAGTCTCCAGTGCCGTGC
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For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DE007AB10QP1&c=7021.f.
Location/Qualifiers
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NNR HISCHKCPDGLHSLFLDLNYNNLDEPPTAI KTLSNLKELGFHSNNI SE I PERA
NNR HISLITHRYDNI QFVQVSARPQHLPELRTLINGASHITEFPHLTGTATLESLT
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49 (MGD|MGI:1341817, GB|NM_010195, evidence: BLASTN, 99%,
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Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Pred. No. 7.4e-234;
0; Mismatches 163;
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                                                                                                   HTC 03-APR-2004
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
                                                                                              AK047873
Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
library, clone:Cl30018C02 product:G protein-coupled receptor 49,
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length DNAs

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Adachi, J. Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Katoh, H., Kawai, J., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kowai, J., Kojima, Y., Kondo, S., Konno, H., Kowai, J., Kojima, Y., Kondo, S., Konno, H., Kawai, J., Sasukawa, T., Katoh, H., Savai, J., Salai, K., Salai, K., Sakazume, N., Sano, H., Sakai, C., Sakai, K., Shinagawa, A., Sakai, C., Sakai, K., Shinagawa, A., Shiraki, T., Sakai, C., Sakai, K., Shinagawa, A., Takaku, T., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, Muramatsu, M., and Hayashizaki, Y. Toya, T., Yasunishi, A., Direct Submission, V., Sano, V., Sano,
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, T., Ohara, E., Watshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J. Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
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Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230.0045, Japan (R-mail:genome-res@gsc.riken.jp, WIR:http://genome.gsc.riken.jp, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue type="heart"
'clone lib="RIKEN full-length enriched mouse cDNA library"
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Please visit our web site for further details.
URL:http://gancome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="D830026M09"
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/mol_type="mRNA"
/strain="C57BL/6J"
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Mus musculus 16 days neonate heart CDNA, RIKEN full-length enriched library, clone:D830026M09 product:CDNA FLJ14471 FIS, CLONE MAWAL1001030, WEAKLY SIMILAR TO LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR homolog [Homo sapiens], full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1110 CCTTCTCTTATCACAATACACTTCTATGACAACCCCATCCAATTTGTTGGAGTATCTGCT 1169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      990 TTAAATTATAATAACCTTGATGAATTCCCCACTGCAATCAAGACACTCCCAACCTTAAG 1049
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                             CTGCACTCCCTGAGGCACCTGTGGCTAGATGACAATGCTCTCACAGACGTCCCTGTCCAG
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
9277953
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1	032 TCAAACCGTCTGCAATCAGTTACCTAATCTCCAAGTCTTACATCTTACAACCTAT 1091 103	RESULT 9 BG196708 BC005 BCOUS BG196708 BG196708 BG196708 BG196708 BG196708 BG196708 BG196708
	RESULT 8 CK449409 CK4496 CK44496 CK4496 C	Query Match 27.4%; Score 745.2; DB 7; Length 940; Best Local Similarity 86.6%; Pred. No. 7.6e-205; Matches 876; Conservative 0; Mismatches 63; Indels 73; Gaps 2;

900

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720

776

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/tissue_type="Stomach"
/cell type="Floating aggregates"
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/clone line="S2LSNU520"
/clone line="S2LSNU520"
/clone line="S2LSNU520"
/clone line="SQLSNU520"
/clone line="SQLSNU52
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BM795259
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481 GTGTGGACCATAGCAGTTCTGGCACTTACTTGTAATGCTTTGGTGACTTCAACAGTTTTC
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Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4410
Fax: +82-42-860-4409
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Unpublished (2002)
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/db_xref="taxon:9606"
/clone="S21SNU520-31-C01"
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Plate: 31 row: C column: 01
High quality sequence stop: 671.
Location/Qualifiers
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Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Offenbacher, J., Danzig, J. and Ducar, M., Hess, J., Cothren, K., Lo, K., Creation of genome-wide protein expression libraries using random activation of gene expression activation of general activation activation of general activation activation activation of general activation activ
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/mol type="mcMu" correction
/db xref="taxon:9606"
/cell line="HT1080"
/clone_lib="Atherses RAGE Library"
/clone_lib="Atherses RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
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/organism="Homo sapiens"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: scain@athersys.com
                                              GI:13718395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Scott J. Cain
                                                                                                                 sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              796; Conservative
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CDNA was synthesized from oligo dT-selected mRNA by parining with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The CDNA vector was circularized with B. coli DNA ligase after digestion of BCORI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells B. coli Topilof' by electroporation method. The CDNA libraries constructed by this method are full-length enriched cDNA library."
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AUTHORS (Lambers) R. 1. Feighbold R. 4. Gordse, L. 1. Berge, J. C. 1.

AUTHORS (Lambers) R. 1. Feighbold R. 4. Gordse, L. 1. Berge, J. C. 1.

AUTHORS (Lambers) R. 1. Feighbold R. 4. Gordse, L. 1. Berge, J. C. 1.

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ALIGCHAIC R. 7. Zeberge B. Berger, C. 1. Remmen, C. M. 1. Schlick, C. D. Altechnic, E. 1. Zeberge, B. Berger, M. 1. Schlick G. M. Hong, L. 1.

BIRCHERON, H. 1. Periods, E. 1. Berger, B. 1. Gards, A. 1. Man, G. M. Hong, L. 1.

Supplement, R. 1. Think, M. 1. Man, M. 1. Man, G. M. Hong, L. 1.

Supplement, R. 1. Markel, A. 4. Gunstants, P. M. McDards, G. M. Hong, L. 1.

Supplement, R. 1. Markel, A. M. Gardia, A. M. Gay, L. J. Hilk, S. M. 1.

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Referran, Y. 1. Malk, M. S. Gardia, A. M. Gay, L. J. Hilk, S. M. 1.

Burker, M. 2. Markel, M. S. Markelman, M. Madan, A. Rodrigues, S. 2.

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Burker, M. M. Millany, M. Madan, M. Modia, M. Rodrigues, S. 2.

Burker, M. M. Millany, M. Madan, M. Modia, M. M. Green, S. D. 1.

Burker, M. M. Man, M. 1. Man, M. M. 1. Markel, M. M. 1. Man, M. 1. M
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Best Local Similarity 57.1%; Pred. No. 3.4e-180;
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is TTATTGAAGT. This library was created for the University lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."
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/mol_type="mRNA"

/mol_type="mRNA"

/mol_type="mRNA"

/db xref="taxon:10090"

/clone="INAGE:30617906"

/tissue_type="whole eye"

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Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
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11 (hases 1 to 763)
12 (hases 1 to 763)
13 (hases 1 to 763)
14 hGC http://mgc.nci.nih.gov/.
16 (hglth, Mammalian Gene Collection (MGC) Unpublished (1999)
17 (contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                2304 GTGAGGCACGTGGCCTCGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTC
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CF742674.1 GI:37639013
EST.
       TACATGGTCGCTCTCATCTTGCTCAATTCCCTTTTGCTTCCTCATGATGACCATTGCCTAC
                                                                         2184 TTCACCGTGGCCCTGGTGATGATCCTTCTGTTTCCTGGTCGTGGCCGGTGCTAC
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                           AK044357
3035 bp mRNA linear HTC 03-APR-2004
Mus musculus adult retina cONA, RIKEN full-length enriched library,
clone:A930009A08 product:G PROTEIN-COUPLED RECEPTOR LGR4 homolog
[Rattus norvegicus], full insert sequence.
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 tull-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3035)
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                                                                                                                        Chordata, Craniata, Vertebrata, Euteleostomi,
Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                              Contact: Genoscope Genorate National de Sequencage edex - FRANCE 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Ist strand cDNA was primed with a NotI-oligo(dI) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSDORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                        For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS2AAW3ZE04_AW9ZA03_1&c=10101.f. Location/Qualifiers
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Parll.-length CDNA libraries and normalization Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30619059.
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                                                                                                                                                                                                                                                                                                                                                                                     prepare mouse tissues.

Retina RNA was provided by Dr. Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is gratefully acknowledged. Please visit our web site for further details.

URL:http://ganome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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HTHLSDHLSTVIRGASIVQWFPNLAGTVHLESLITGTKISSIPDDLCONGWALTATLD
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VSNLLAGIYTGILTFLDAVSNGRFAEFGIWWETGSGCKVAGSLAVFSSESAVFLITLA
                                                                                                                   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIREN), imboratory for Genome Exploratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, WRL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVERSVFAKDVMKNGKSSHLRQFQVAALVALLGAAIAGCFPLFHGGQYSASPLCLPFP
TGETPSLGFTVTLVLLNSLAFLLMAIIYTKLYFNLEKEDPSENSQSSMIKHVAMLIFT
NCIFFCPVAFFSFAPLITAISISPEIMKSVTLIFPPLPACLNPVLYVFFNPKFKDDWK
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CFYQSRGFPLVRYAYNLPRVRD"
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'clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136
                                                                                                                                                                                                                                                                                       CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321
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Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
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Pred. No. 1.8e-155;
0; Mismatches 991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="adult"
<1. .2638
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larity 54.5%;
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E 1 (Dases 1 to 590)

S Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes

L Genomics 84 (1), 205-210 (2004)

Contact: Fu GK

Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102

Email: gfu@incyte.com.
Location/Qualifiers
                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GITCITATGCTGCAGAATAATCAGCTAAGACACGTACCCACAGAAGCTCTGCAGAATTTG
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  mRNA line
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|/db xref="taxon:9606"
|/clone_lib="FLP"
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                                                AAGAAAGATGCTGGAATGTTTCAGGCTCAAGATGAACGTGACCTTGAAGATTTCCTGCTT
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